

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
1 May 2003 (01.05.2003)

PCT

(10) International Publication Number
WO 03/035621 A1

- (51) International Patent Classification⁷: C07D 209/14, 215/14, A61K 31/404, 31/47
- (21) International Application Number: PCT/US02/33660
- (22) International Filing Date: 19 October 2002 (19.10.2002)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
60/336,191 22 October 2001 (22.10.2001) US
60/410,726 13 September 2002 (13.09.2002) US
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- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:
— with international search report
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*



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(54) Title: PROTEIN KINASE AND PHOSPHATASE INHIBITORS, METHODS FOR DESIGNING THEM, AND METHODS OF USING THEM

(57) Abstract: The present invention provides a method for identifying inhibitors of protein kinases and/or protein phosphatases. Methods are also provided for inhibiting protein kinase and/or protein phosphatase activity. Specific non-peptide protein tyrosine kinase and/or protein phosphatase inhibitors are provided. The protein kinase or protein phosphatase inhibitors of the present invention may be used to treat a number of conditions in patients, including cancer, psoriasis, arthrosclerosis, immune system activity, diabetes, or obesity. In addition, the present invention provides a method for protecting against or treating hearing loss in a subject. This method involves administering an effective amount of a protein tyrosine kinase inhibitor to the subject to protect against or to treat hearing loss.

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**PROTEIN KINASE AND PHOSPHATASE INHIBITORS,
METHODS FOR DESIGNING THEM, AND METHODS OF USING THEM**

5 The present application claims the benefit of U.S. Provisional Patent Application Serial No. 60/336,191, filed October 22, 2001, and U.S. Provisional Patent Application Serial No. 60/410,726, filed September 13, 2002, which are hereby incorporated by references in its entirety. The subject matter of this application was made with support from NIH/NIDCD (Grant Nos. P01-DC03600 and 1R21DC04984-
10 01). The U.S. Government may have certain rights in this invention.

BACKGROUND OF THE INVENTION

Protein kinases are a large class of enzymes which catalyze the transfer of the
15 γ -phosphate from ATP to the hydroxyl group on the side chain of Ser/Thr or Tyr in proteins and peptides and are intimately involved in the control of various important cell functions, perhaps most notably: signal transduction, differentiation, and proliferation. There are estimated to be about 2,000 distinct protein kinases in the human body (Hunter, 1987, 1994, Hanks & Hunter, 1995), and although each of these
20 phosphorylate particular protein/peptide substrates, they all bind the same second substrate ATP in a highly conserved pocket. Protein phosphatases catalyze the transfer of phosphate in the opposite direction.

Inhibitors of various known protein kinases or protein phosphatases could have a variety of therapeutic applications provided sufficient selectivity, and
25 acceptable *in vivo* pharmacological properties, can be incorporated into such inhibitors (Levitzi, 1996a). Perhaps the most promising potential therapeutic use for protein kinase or protein phosphatase inhibitors is as anti-cancer agents. This potential application for protein tyrosine kinase ("PTK") inhibitors has been highlighted in many recent reviews (e.g. Lawrence & Hiu, 1998, Kolibaba & Druker,
30 1997, Showalter & Kraker, 1997, Patrick & Heimbrook, 1996, Groundwater et al., 1996, Levitzi, 1995). The foundation for this application is based partly upon the fact that about 50% of the known oncogene products are PTKs and their kinase activity has been shown to lead to cell transformation (Yamamoto, 1993).

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The PTKs can be classified into two categories (Courtneidge, 1994), the membrane receptor PTKs (e.g. growth factor receptor PTKs) and the non-receptor PTKs (e.g. the Src family of proto-oncogene products). There are at least 9 members of the Src family of non-receptor PTK's with pp60^{c-src} (hereafter referred to simply as "Src") being the prototype PTK of the family wherein the ca. 300 amino acid catalytic domains are highly conserved (Rudd et al., 1993, Courtneidge, 1994). The hyperactivation of Src has been reported in a number of human cancers, including those of the colon (Mao et al., 1997, Talamonti et al., 1993), breast (Luttrell et al., 1994), lung (Mazurenko et al., 1992), bladder (Fanning et al., 1992), and skin (Barnekow et al., 1987), as well as in gastric cancer (Takeshima et al., 1991), hairy cell leukemia (Lynch et al., 1993), and neuroblastoma (Bjelfman et al., 1990). Overstimulated cell proliferation signals from transmembrane receptors (e.g. EGFR and p185HER2/Neu) to the cell interior also appears to pass through Src (Mao et al., 1997, Parsons & Parsons, 1997, Bjorge et al., 1996, Taylor & Shalloway, 1996). Consequently, it has recently been proposed that Src is a universal target for cancer therapy (Levitzki, 1996), because its' hyperactivation (without mutation) is involved in tumor initiation, progression, and metastasis for many important human tumor types.

In view of the large, and growing, potential for inhibitors of various protein kinases and protein phosphatases, a variety of approaches to obtaining useful inhibitors is needed. The status of the discovery of PTK inhibitors (Lawrence & Niu, 1988, Showalter & Kraker, 1997, Patrick & Heimbrosk, 1996, Groundwater et al., 1996, Budde et al., 1995, Levitzki & Gazit, 1995; Frame, 2002; Sawyer et al., 2001; Haskell et al., 2001, Martin, 2001; Bridges, 2001; Blume-Jensen et al., 2001; Biscardi et al., 2000; Susa & Teti, 2000; Susa et al., 2000; Irby et al., 2000; Schlessinger, 2000; Abram et al., 2000; Garcia-Echeverria et al., 2000; Sedlacek, 2000; Sridhar et al., 2000; Biscardi et al., 1999) has been extensively reviewed. Random screening efforts have been successful in identifying non-peptide protein kinase inhibitors but the vast majority of these bind in the highly conserved ATP binding site. A notable recent example of such non-peptide, ATP-competitive, inhibitors are the 4-anilinoquinazolines, and analogs, which were shown to be effective against the epidermal growth factor receptor PTK (EGFR PTK) (e.g. Rewcastle et al., 1996).

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Although this class of inhibitors was reported to be selective for the EGFR PTK vs. six other PTKs (including Src, Fry et al., 1994) it is unknown what their effect is on most of the remaining 2,000 protein kinases that all bind ATP as well as a large number of other ATP, ADP, GTP, GDP, etc. utilizing proteins in the body.

5 Therefore, potential side effects from PTK inhibitor drugs that mimic ATP, which might only be discovered after expensive animal toxicity studies or human clinical trials, are still a serious concern. Also, although this class of compounds was a nice discovery and is undergoing further exploration, they do not provide a rational and general solution to obtaining non-peptide inhibitors for any desired PTK, e.g. in this
10 case Src. The risk of insufficient specificity *in vivo* with ATP-competitive PTK inhibitors has also been noted by others, along with the inherent three order of magnitude reduction in potency these inhibitors display when competing with the mM levels of intracellular ATP rather than the μ M levels used in the isolated enzyme assays (e.g. see Lawrence & Niu, 1998, Hanke et al., 1996, Kelloff et al., 1996).

15 An older, and more extensively studied, class of non-peptide PTK inhibitors is erbstatin and the related tyrphostins (see reviews). This class of inhibitors are active against the receptor PTKs and their mode of inhibition is complex but does not appear to involve binding in the peptide substrate specificity site regions of the active site (Hsu et al., 1992, Posner et al., 1994). Furthermore, they are inactive against the
20 isolated PTK when the *unnatural* assay metal Mn^{2+} is replaced with the *natural* Mg^{2+} (Hsu et al., 1992), are chemically unstable (Budde et al., 1995, Ramdas et al., 1995 & 1994), and are known to be cytotoxic to normal and neoplastic cells by cross-linking proteins (Stanwell et al., 1995 & 1996) as well as inhibit cell growth by disrupting mitochondria rather than PTK inhibition (Burger et al., 1995).

25 An important contribution to the protein kinase field has been the x-ray structural work with the serine kinase cAMP-dependent protein kinase ("PKA") bound to the 20-residue peptide derived from the heat stable inhibitor protein, PKI(5-24), and Mg_2ATP (Taylor et al., 1993). This structural work is particularly valuable because PKA is considered to be a prototype for the entire family of protein kinases
30 since they have evolved from a single ancestral protein kinase. Sequence alignments of PKA with other serine and tyrosine kinases have identified a conserved catalytic core of about 260 residues and 11 highly conserved residues within this core (Taylor

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et al., 1993). Two highly conserved residues of particular note for the work proposed herein are the general base Asp-166 which is proposed to interact with the substrate OH and the positively charged residue, Lys-168 for serine kinases and an Arg for tyrosine kinases (Knighton et al., 1993), which is proposed to interact with the γ -phosphate of ATP to help catalyze transfer of this phosphate. Two additional important PKA crystal structures have been reported (Madhusudan et al., 1994), one for the ternary PKA:ADP:PKI(5-24) complex wherein the PKI Ala 21 has been replaced with Ser (thereby becoming a substrate), and one for the binary PKA:PKI(5-24) complex wherein the PKI Ala 21 has been replaced with phosphoserine (an end product inhibitor). The ternary complex shows the serine OH donating a H-bond to Asp-166 and accepting a H-bond from the side chain of Lys 168. The binary complex shows the phosphate group of phosphoserine forming a salt bridge with the Lys-168 side chain and within H-bonding distance of the Asp-166 carboxyl group. These structures support the earlier proposed roles for Asp-166 and Lys-168 in the catalytic mechanism.

The x-ray structures of PKA show that the enzyme consists of two lobes wherein the smaller lobe binds ATP and the larger lobe the peptide substrate. Catalysis occurs at the cleft between the lobes. The crystallographic and solution structural studies with PKA have indicated that the enzyme undergoes major conformational changes from an "open" form to the "closed" catalytically active form as it binds the substrates (Cox et al., 1994). These conformational changes are presumed to involve the closing of the cleft between the two lobes as the substrates bind bringing the γ -phosphate of ATP and the Ser OH in closer proximity for direct transfer of the phosphate.

However, many inhibitors of protein kinases and protein phosphatases still lack the specificity and potency desired for therapeutic use. Due to the key roles played by protein kinases and protein phosphatases in a number of different diseases, including cancer, psoriasis, atherosclerosis, Type II diabetes, obesity, and their role in regulating immune system activity, inhibitors of specific protein kinases and protein phosphatases are needed. The present invention provides a novel approach for designing protein kinase and/or protein phosphatase inhibitors and the resulting protein kinase and/or protein phosphatase inhibitors, which may be more specific for

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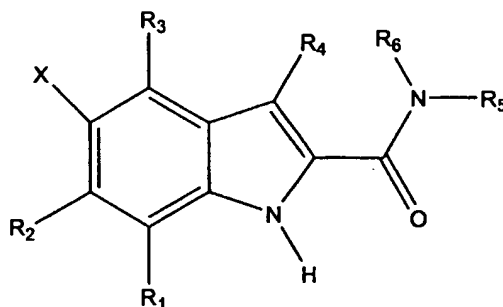
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the targeted pathways. The present also provides a novel approach for protecting against or treating hearing loss.

SUMMARY OF THE INVENTION

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The invention provides a non-peptide protein tyrosine kinase inhibitor and/or protein phosphatase inhibitor having the formula:



- 10 wherein X is a halogen, and R₁ through R₆ may be the same or different, and are selected from the group consisting of H, C(O)R_a, C(O)NR_aR_b, C(O)OR_a, C(O)SR_a, OH, OR_a, OC(O)R_a, OC(O)OR_a, NH₂, NR_aR_b, NR_aC(O)R_b, NR_aC(O)NR_bR_c, NR_aC(O)OR_b, NR_aC(O)SR_b, NR_aS(O)R_b, NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b, NR_aP(O)OR_bOR_c, NR_aP(O)OR_bR_c, NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a,
 15 S(O)OR_a, S(O)₂OR_a, S(O)NR_aR_b, S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic, or unbranched), preferably having from 1 to 20 carbon atoms, optionally containing a double or triple bond and optionally substituted with a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide,
 20 thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl, or R₅ and R₆ together form a heterocyclic compound. R_a, R_b, and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic, or unbranched),
 25 optionally substituted with a heteroatom or other functional groups such as a

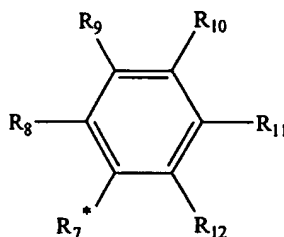
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carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions.

In one embodiment, at least one of R_5 or R_6 is



- wherein R_7^* is the point of attachment and is $(CH_2)_x$, wherein x is from 0 to 10,
- 10 CH_2CHOH , $CH(CH_3)R$, or $CH(CH_3)S$, and each of R_8 through R_{12} may be the same or different and are selected from the group consisting of H , $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH , OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic, or unbranched), preferably having from 1 to 20 carbon atoms, optionally containing a double or triple bond and optionally substituted with a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester,
- 20 alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H , aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic, or unbranched), optionally substituted with a heteroatom
- 25 or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid,

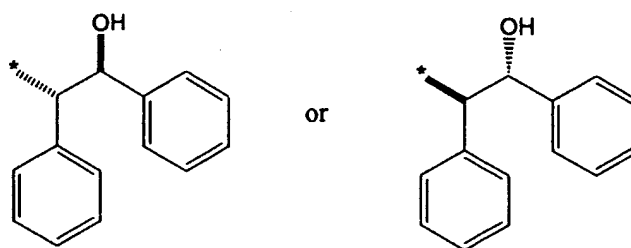
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phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that any of R_8 through R_{12} can be substituted or unsubstituted.

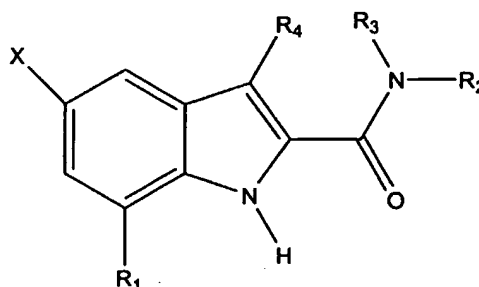
In another embodiment, at least one of R_5 or R_6 is



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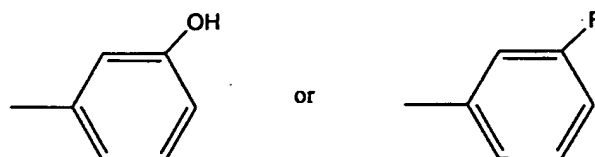
wherein the asterisk indicates the point of attachment to the nitrogen.

The present invention also provides a non-peptide protein tyrosine kinase inhibitor and/or protein phosphatase inhibitor having the formula:



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wherein X is a halogen, preferably, fluorine, and R_1 through R_4 are specificity side chain elements. In one embodiment, R_1 is H, R_2 is



R_3 is H, and R_4 is H. The compound may also be substituted at any other position on the indole ring.

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The present invention provides a method for identifying inhibitors of protein kinases. The method involves providing at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein kinase, wherein at least one of the one or more functional groups is a halogen, combining at least one first module with at least one second module which provides a non-peptide scaffold to form one or more combinations of the first and second modules, screening the one or more combinations of the first and second modules for protein kinase inhibition, and selecting combinations of the first and second modules which inhibit protein kinase activity. As used herein, a module is a single molecular entity or a collection of functional groups. As used herein, a non-peptide scaffold is a molecule which may include peptide bonds, so long as a part of the molecule is not a peptide.

The present invention also provides a method of inhibiting a protein kinase. The protein kinase is contacted by a compound comprising at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein kinase, wherein the one or more functional groups comprise a halogen, and a second module which provides a non-peptide scaffold. The combination of at least one first module and second module inhibits the protein kinase activity.

In yet another embodiment, the present invention provides a method of treating a condition, responsive to a protein kinase inhibitor, in a subject. A protein kinase inhibitor is administered to a subject. The protein kinase inhibitor has at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein kinase, wherein the one or more functional groups comprise a halogen, and a second module which provides a non-peptide scaffold. The combination of at least one first module and second module inhibits protein kinase activity in the subject.

In a further embodiment, the present invention provides a method for identifying inhibitors of protein phosphatases. The method involves providing at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein phosphatase, combining at least one first module with at least one second module which provides a non-peptide

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scaffold to form one or more combinations of the first and second modules, screening the one or more combinations of the first and second modules for phosphatase inhibition, and selecting combinations of the first and second modules which inhibit protein phosphatase activity.

5 Another aspect of the present invention is a method of inhibiting a protein phosphatase. The protein phosphatase is contacted by a compound comprising at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein phosphatase, and a second module which provides a non-peptide scaffold. The combination of at
10 least one first module and second module inhibits the protein phosphatase activity.

In yet another embodiment, the present invention provides a method of treating a condition, responsive to a protein phosphatase inhibitor, in a subject. A protein phosphatase inhibitor is administered to a subject. The protein phosphatase inhibitor has at least one first module having one or more functional groups each
15 capable of covalently or non-covalently binding to catalytic residues of the protein phosphatase, and a second module which provides a non-peptide scaffold. The combination of at least one first module and second module inhibits protein phosphatase activity in the subject.

The present invention also relates to a method for protecting against or treating
20 hearing loss in a subject. This method involves administering an effective amount of a protein tyrosine kinase inhibitor to the subject to protect against or to treat hearing loss.

In accordance with the method of protecting against or treating hearing loss of the present invention, a low concentration of protein tyrosine kinase inhibitor can be
25 administered to the subject to achieve the desired effect. In addition, the protein tyrosine kinase inhibitors disclosed herein exhibit low toxicity and, therefore, are suitable for treatment of hearing loss. Further, the protein tyrosine kinase inhibitors can be administered an amount effective to protect against or treat hearing loss, as well as to treat other disorders responsive to protein kinase inhibitors, such as cancer,
30 psoriasis, atherosclerosis, or immune system activity. In particular, the protein tyrosine kinase inhibitors may provide a synergistic effect with certain cancer drugs. For example, promising inhibitors can be screened in primary human tumor tissue

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assays, particularly to look for synergy with other known anti-cancer drugs. In addition, the protein kinase inhibitors may reduce toxicity of certain cancer drugs (e.g., platinum-based drugs which are toxic to the cochlea and kidney), thereby allowing increased dosage.

5

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts the modular strategy for developing non-peptide protein kinase inhibitors. Step 1 utilizes one or more first modules ("M₁'s") to identify promising non-peptide scaffolds. Step 2 enhances the potency by adding specificity elements. During this step the scaffolds are validated. Whether the inhibitor is non-ATP competitive can also be determined. In step 3, the potency and selectivity are further enhanced using combinatorial libraries to optimize M₁ and specificity elements.

15 Figure 2 provides a depiction of the x-ray structure of (PKA):Mg₂ATP:pseudosubstrate inhibitor.

Figure 3 provides a general module M₁ design features for binding to the conserved protein kinase catalytic region.

Figure 4 shows that the boronic acid "inhibitors" 21 and 22 were shown to be substrates for PKA.

Figure 5 demonstrates the binding interactions of Src substrate Ac-Ile-Tyr-Gly-Glu-Phe-NH₂ (SEQ. ID. No. 1) in model Src active site.

Figure 6 shows the design of naphthalene-based Src inhibitor scaffolds.

Figure 7 shows the design of isoquinoline and indole-based Src inhibitor scaffolds.

Figure 8 provides an example of the chemistry used to prepare the naphthalene inhibitors, which is described in Marsilje 2000. A boronic acid functionality can be put in place of a M₁ hydroxyl groups in the Src inhibitors from Table V using the Pd(0)-catalyzed cross-coupling methodology wherein either an aryl triflate (Ishiyama et al, 1997) or an aryl halide (Ishiyama, 1995) can be coupled with the commercially available pinacol ester of diboron.

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Figure 9 shows a synthetic scheme that can be followed, in order to attach hydrophobic S₂ selectivity elements to the naphthalene scaffold.

Figure 10 shows successful model reactions with naphthalene chemistry, which can be converted to the solid phase in preparation for synthesizing
5 combinatorial libraries of this scaffold in a 96-well plate format. The chemistry has been carried out on the less active naphthalene regioisomer represented by 44 because this compound is readily obtained from commercially available 3,5-dihydroxy-2-naphthoic acid, as described in Marsilje 2000.

Figure 11 provides a possible strategy for modifying the naphthalene scaffold
10 in combinatorial libraries.

Figure 12 shows the conversion of the triflate functionality formed in reaction 2 from intermediate 69 (Figure 11) to an amine (Wolfe et al, 1997) and then a series of amides or other amine derivatives.

Figure 13 shows modeling a series of hydroxy-containing analogs of the
15 boronic acid M₁ group shown in the Src and IRTK (insulin receptor protein tyrosine kinase) active sites.

Figure 14 shows results from testing of the non-peptide Src inhibitor 43-meta (Table V) in the LA25 and NRK cell lines.

Figure 15 is a graph showing the maximum tolerated dose (MTD) of two Src
20 inhibitors (1a from Example 1 and 2k from Example 4) in SCID mice.

Figure 16A shows a comparison of taxol and doxorubicin (they were more effective than etoposide and cisplatin in this tumor cell culture) with the three Src inhibitors (45, 43-meta, and 49-meta from Table V) utilizing ovarian tumor cells from tumor N015. Figure 16B shows the results from tests of the Src inhibitors for
25 inhibition of normal human fibroblast cell growth. No inhibition of normal cell growth (both subconfluent and confluent; some enhanced growth was observed instead) was found, indicating that these inhibitors are not toxic to normal cells even at a 10-fold higher concentration. Figure 16C shows the results from tests of two of the Src inhibitors for inhibition of *ts* v-Src stimulated LA25 cell growth. Figure 16D
30 shows the results from tests of two of the Src inhibitors for inhibition of normal rat kidney cell growth. Figure 16E provides the structures of the Src inhibitors 45, 43-meta, and 49-meta.

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Figures 17A-B are graphs showing *in vitro* cytotoxicity of malignant prostate PC-3-LN cells with a range of each of four Src protein tyrosine kinase inhibitors and one inactive control (KLM 2-25).

Figures 18A-B show Western analyses of proteins in malignant PC-3-LN prostate cancer cells treated with 45 and detected using either anti-phosphotyrosine (Figure 18A) or anti-paxillin (Figure 18B) antibodies.

Figure 19 is a graph showing the quantitation of two distinct phosphorylated substrates for focal adhesion complex (paxillin and p130 cas) and a third unknown substrate.

Figure 20 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise prior to experimental manipulation.

Figure 21 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 0.5 kHz band noise at day 0, day 1, day 3, and day 20 after experimental manipulation.

Figure 22 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 1 kHz band noise at day 0, day 1, day 3, and day 20 after experimental manipulation.

Figure 23 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 2 kHz band noise at day 0, day 1, day 3, and day 20 after experimental manipulation.

Figure 24 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 4 kHz band noise at day 0, day 1, day 3, and day 20 after experimental manipulation.

Figure 25 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 8 kHz band noise at day 0, day 1, day 3, and day 20 after experimental manipulation.

Figure 26 is a graph showing the average dB threshold shifts (dB) in chinchilla cochleas at day 20 for control and treated ears.

Figure 27 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise prior to experimental manipulation.

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Figure 28 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise on day 1 after experimental manipulation.

Figure 29 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise on day 3 after experimental manipulation.

Figure 30 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise on day 7 after experimental manipulation.

Figure 31 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise on day 20 after experimental manipulation.

Figure 32 is a graph showing average threshold shifts (dB) in chinchilla cochleas after exposure to 8000 Hz on day 1, day 3, day 7, and day 20.

Figures 33A-F are SEM images of chinchilla cochleas. Figure 33A shows a split (marked by S) of the reticular lamina after exposure to an impulse noise. Figure 33B shows focal adhesion kinase (FAK) staining in a cochlea exposed to an octave band noise (OBN) centered at 4 kHz at 105 dB (SPL). Figure 33C shows a small lesion with a few apoptotic nuclei (marked with arrow) from a cochlea exposed to an OBN at 110 dB. Figure 33D shows FAK staining for the lesion shown in Figure 33C. Figure 33E shows a confocal scanning level a few microns lower than in Figure 33D, demonstrating that the lesion extends well below the cuticular plate and into the cell body (marked with arrow). Figure 33F shows FAK staining in a cochlea exposed to impulse noise at 155 dB (SPL). In this figure, many outer hair cells have lost their cuticular plate integrity. The remaining outer hair cells show strong FAK fluorescence in the cuticular plates.

Figures 34A-B are confocal images of chinchilla cochleas exposed to high level noise. In Figure 34, the chinchilla cochlea was pre-treated with 1a (see Table VI, Example 1). In Figure 34B, the chinchilla cochlea was left untreated.

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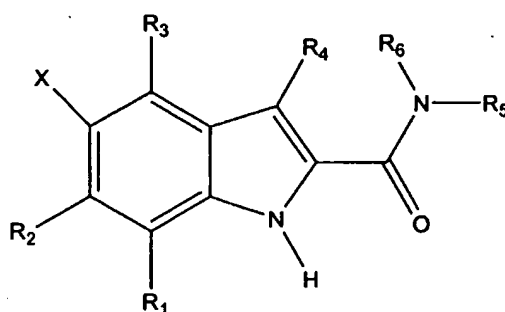
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DETAILED DESCRIPTION OF THE INVENTION

The present invention provides inhibitors of protein kinases and/or protein phosphatases. In one embodiment, the protein kinase and/or protein phosphatase inhibitor is a non-peptide inhibitor having the following formula:



wherein X is a halogen, and R₁ through R₆ may be the same or different, and are selected from the group consisting of H, C(O)R_a, C(O)NR_aR_b, C(O)OR_a, C(O)SR_a,
 10 OH, OR_a, OC(O)R_a, OC(O)OR_a, NH₂, NR_aR_b, NR_aC(O)R_b, NR_aC(O)NR_bR_c,
 NR_aC(O)OR_b, NR_aC(O)SR_b, NR_aS(O)R_b, NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b,
 NR_aP(O)OR_bOR_c, NR_aP(O)OR_bR_c, NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a,
 S(O)OR_a, S(O)₂OR_a, S(O)NR_aR_b, S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl,
 heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic,
 15 or unbranched), preferably having from one to 20 carbon atoms, optionally containing
 a double or triple bond and optionally substituted with a heteroatom or other
 functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether,
 thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid,
 phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl,
 20 biaryl, and heterobiaryl, or R₅ and R₆ together form a heterocyclic compound. R_a, R_b,
 and R_c can be the same or different and are selected from the group consisting of H,
 aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic, or unbranched),
 optionally substituted with a heteroatom or other functional groups such as a
 carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea,
 25 urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid,

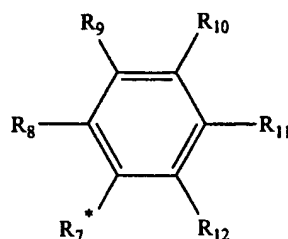
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phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions. Examples of suitable R groups are provided in Table VI, below.

In one embodiment, at least one of R_5 or R_6 is



5

wherein R_7^* is the point of attachment and is $(CH_2)_x$, wherein X is from 0 to 10, CH_2CHOH , $CH(CH_3)R$, or $CH(CH_3)S$, and each of R_8 through R_{12} may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic, or unbranched), preferably having from one to 20 carbon atoms, optionally containing a double or triple bond and optionally substituted with a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic, or unbranched), optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions.. In a preferred embodiment, each of R_8 through R_{12} is selected from the group consisting of OCH_3 , OCH_2CH_3 , H, CH_3 ,

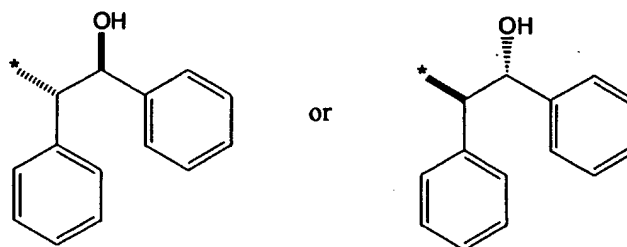
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OH, CH₂OH, CF₃, OCF₃, CFO, C₆H₅, OC₆H₅, OCH₂C₆H₅, OCH₂CH₂CH₃, CHO, CO₂H, CO₂CH₃, CH₂CO₂H, CH₂CO₂CH₃, NO₂, and halogen.

In another embodiment, at least one of R₅ or R₆ is

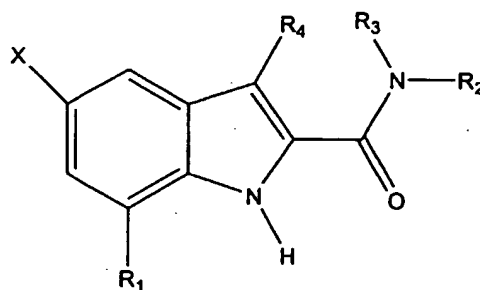


5 wherein the asterisk indicates the point of attachment to the nitrogen.

In a preferred embodiment, the non-peptide inhibitor inhibits the activity of pp60^{c-src} tyrosine kinase, pp56^{lck} tyrosine kinase, or pp55^{lyn} tyrosine kinase.

In another preferred embodiment, the non-peptide inhibitor inhibits the activity of protein tyrosine phosphatase 1B (PTP-1B).

10 Another non-peptide protein tyrosine kinase and/or protein phosphatase inhibitor of the present invention has the following formula:



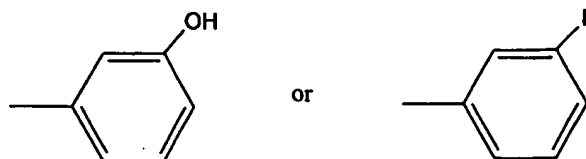
15 wherein X is a halogen, preferably, fluorine, and R₁ through R₄ are specificity elements. As used herein, specificity elements or specificity side chains are side chains which will bind in unique binding pockets for individual protein kinases. Thus, the side chains used will depend on the particular protein kinase or protein phosphatase to be inhibited. To identify suitable side chains, known peptide binding side chains may be used to identify analogues which are then used in combinatorial
20 chemistry techniques to expand the library of possible side chains.

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In one embodiment, R₁ is H, R₂ is



R₃ is H, and R₄ is H. The compound may also be substituted at any other position on the indole ring.

- 5 The compounds of the present invention provide activity against tyrosine kinases, such as pp60^{c-src}, and are expected to improve the ability of the compound to inhibit tyrosine kinases *in vivo*, since one easily metabolized OH group has been removed. In particular, an OH group at the 5-position on the indole ring has been substituted with a halogen. The halogen is a hydrogen bond acceptor, useful with
- 10 catalytic residues which are hydrogen bond donors. In addition, the halogen is not metabolized in phase II metabolism and is electronegative, leading to *in vivo* benefits (see, e.g., Park et al., 2001). Some members of this class are also inhibitors of the opposing enzymes, i.e., phosphotyrosine phosphatases. These compounds are inhibitors of pp60^{c-src}, of highly metastatic prostate cancer cell growth, and are non-
- 15 toxic in mice upon high dose acute i.p. administration, as described in Example 1, below. Some of these compounds may be found to have other biological activities upon broader testing (e.g., inhibit glycogen phosphorylase for Type II diabetes, HIV reverse transcriptase, or thromboxane synthase). Thus, these compounds may be used as tyrosine kinase inhibitors for therapeutic applications, such as cancer. Tyrosine
- 20 kinase inhibitors have other potential therapeutic applications as well (e.g., immunosuppressants in the case of p56lck) and inhibitors of the tyrosine phosphatase PTP-1B may provide drugs for treating Type II diabetes or obesity.

 The present invention also provides a method for identifying inhibitors of protein kinases. The general modular strategy for the development of non-peptide

25 PTK inhibitors is outlined in Figure 1. Basically, at least one first module having a one or more functional groups for binding to catalytic residues of the protein kinase (in a preferred embodiment, at least one of the functional groups is a halogen) is combined with at least one second module which provides a non-peptide scaffold.

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The functional group(s) of the at least one first module are each capable of covalently or non-covalently binding with catalytic residues of the protein kinase. Thus, each functional group of each first module is capable of reversible or irreversible bond formation, either covalently or non-covalently, to catalytic residues of the protein kinase when the protein kinase the first module are combined under conditions effective for such binding. Combinations of the first and second modules which inhibit protein kinase activity are then selected. Step 1 begins with protein kinase inhibitor information which was already generated, i.e. pentapeptide scaffolds which bind in the substrate specificity sites of PKA or Src have already been used to position various rationally designed functional groups (i.e. module "M₁" or "first module") to interact with the conserved catalytic residues, MgATP or MgADP. A selection of preferred functional groups have now been identified in this fashion to serve as the initial M₁ module for Step 1. These M₁ functional groups have been utilized to identify promising non-peptide scaffolds for Src inhibitors in Step 1. It was anticipated that these bare non-peptide scaffolds, with only an M₁ appendage, would have low binding affinity and be relatively non-selective among the protein tyrosine kinases (PTKs). A lack of selectivity at the level of Step 1 is viewed as an advantage for the development of a general strategy which can be reapplied to additional PTKs. Therefore, the suite of non-peptide scaffolds identified in Step 1 can be recycled for use against additional PTKs by re-screening them and carrying the better ones through Steps 2 and 3, all using the new PTK target. The potency of these bare scaffolds from Step 1 may be increased enough by the attachment of one or two initial specificity elements (S_n) to allow for the validation of the scaffold as non-ATP competitive and amenable to further potency enhancements using combinatorial chemistry in a rationally guided fashion. Promising Src non-peptide M₂ (second module) scaffolds identified in Step 1 have undergone Step 2 and displayed a one to two order-of-magnitude increase in potency against Src as well as non-competitive binding relative to ATP.

Validation of the scaffolds at the level of Step 2 before undertaking the resource intensive combinatorial library synthesis and testing of Step 3 is important for three reasons: 1) to develop the chemistry for appending the specificity element (S_n) side chains; 2) to determine that these inhibitors are not ATP-competitive; and

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3) to determine that the potency is responding to the side chain S_n properties and attachment points as would be expected based upon the working model for the Src:inhibitor complex (this provides some confidence that rationally guided choices can be made for the ranges of individual selectivity elements S_n to include in the focused libraries of Step 3).

It is in Step 3 that high potency and specificity for a particular PTK is anticipated because numerous combinations of M_1 functional groups (and close analogs M_1') with selectivity elements (S_n) will be evaluated experimentally via combinatorial chemistry and high-throughput screening. Potency and selectivity may be further increased if necessary by appending additional specificity elements (see optional S_n 's in Figure 1).

In each of the Steps 1-3, molecular modeling studies with the IRTK:peptide:AMP-PNP crystal structure, the model of the Src:peptide complex and the models for the Src complex with the individual families of inhibitors based upon a particular scaffold will be used as qualitative guides. These modeling studies have been remarkably helpful thus far in guiding the inhibitor design efforts as detailed later. Combining structure-based design and combinatorial chemistry technologies in this fashion provides a synergy wherein the major individual deficiencies of these technologies used in isolation are addressed by the strengths of the other. The major deficiency of structure-based design is the difficulty in quantitatively predicting ligand binding affinities, which is particularly challenging due to the complex effects of solvation and entropy (Ajay & Murcko, 1995). The major strength of structure-based design is its capability to predict what types of molecules are likely to be good ligands. Structure-based design can determine the rough boundaries (proteins have some flexibility which need to be taken into account) for molecular size and shape as well as indicate where hydrophobic, H-bonding, and ionic interactions are likely to occur. On the other hand, the major deficiency of combinatorial chemistry is that "molecular space" for drug-sized molecules (i.e. MW ca. 500 or less) is so large that one could not hope to sample all of this molecular space with a high density of coverage in a reasonable sized combinatorial library. A recent estimate (Bohacek et al., 1996) of the number of possible compounds containing up to 30 atoms chosen only from carbon, nitrogen, oxygen and sulfur (in addition to H's) is 10^{60} compounds.

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This is in the molecular weight range of typical drug molecules and still does not include additional diversity provided by other atoms, e.g. halogens. Consequently, additional constraints need to be used to identify regions of molecular space wherein particular drug candidates are likely to be located. Structure-based design can

5 drastically reduce the volume of molecular space to be explored by identifying the types of molecules which have a higher probability of being good ligands. The inability to quantitatively predict which of these "focused" combinatorial library members will in fact be the tightest binding ligands (i.e. the quantitation problem) is then resolved by employing an efficient combinatorial synthesis and high-throughput

10 testing of the library.

In the earlier peptide based serine and tyrosine kinase inhibitor design efforts, PKA was used as a convenient qualitative model for designing the protein kinase inhibitor module M_1 for interaction with the conserved catalytic residues. There is much more structural and kinetic information available for PKA than any other

15 protein kinase.

The crystal structure of PKA complexed with Mg_2ATP and a pseudosubstrate (i.e. OH replaced with H) peptide inhibitor (PKI 5-24 amide) has been solved (Zheng et al., 1993) and the active site interactions near the P 0 Ala of this inhibitor are shown in Figure 2.

20 This crystal structure shows Mg_2ATP bound to the small lobe of PKA and a 20-residue pseudosubstrate peptide inhibitor bound to the large lobe with the overall conformation of the enzyme in the closed (i.e. the two lobes are touching) and activated state. The distances between the P 0 Ala side chain carbon and the nearby heavy atoms in the complex are shown in Å in Figure 2. These distances show that

25 the Ala side chain is within van der Waals contact distance of the surrounding atoms and indicates that there is little space for appending bulky M_1 functional groups to the Ala side chain. However, PKA is a flexible enzyme with open, closed and intermediate conformations (Cox et al., 1994) and these more open conformations would result in a retraction back of the ATP γ -phosphate from the inhibitor Ala

30 thereby creating a binding cavity for appended M_1 functional groups. Furthermore, PKA binds $MgADP$ with the same affinity as $MgATP$ (Whitehouse et al., 1983) and the ratio of ATP/ADP in cells is typically 10/1 (Alberts, et al. 1994). Therefore, at

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equilibrium, ca. 10% of the cellular protein kinase is in the MgADP bound state and this form of the enzyme can also be targeted with an inhibitor to drain all of the enzyme from the catalytic cycle into a PKA:MgADP:inhibitor inactive complex.

Since the PKA catalytic residues Asp-166 and Lys-168 are completely
5 conserved in all serine kinases, and the tyrosine kinases only differ by the substitution of Arg for Lys-168 (Taylor et al., 1993), this region of the active site was chosen, along with the adjoining MgATP or MgADP, to target a selection of inhibitor functional groups which could serve as M_1 and be broadly useful for developing inhibitors for the entire protein kinase family. By targeting M_1 to the region of the
10 active site adjacent to the nucleotide, an orientation point is provided for the non-peptide inhibitors which can extend into the peptide binding specificity sites without always competing with ATP/ADP binding.

A selection of functional groups which could be utilized as M_1 was identified first because, although this region of the active site is very highly conserved, it was
15 expected that each particular protein kinase will still display some differing preferences across this selection due to small variations in the active site conformations and adjoining residues. Furthermore, the rank order preference among this selection of M_1 's may change somewhat as the M_1 module is appended to different non-peptide scaffolds. This expectation is based upon the potential for each
20 non-peptide scaffold to bind in somewhat different orientations with each individual protein kinase and with each particular set of selectivity element (S_n) side chains. Pentapeptide scaffolds were chosen for the initial screening of functional groups for M_1 because the binding orientation of these larger peptide scaffolds is likely to be very consistent and predictable (i.e. closely resembling that observed by x-ray)
25 throughout the series and could be more confidently assumed to position each tested M_1 functionality adjacent to the conserved catalytic residues as intended. Consequently, the goal of this earlier peptide-based work was to identify a collection of M_1 functional groups which can be used, not only for the initial screening of non-peptide scaffolds (Step 1), but also as an initial set of M_1 side chains which can be
30 further expanded via close analogs and thereby optimized simultaneously with the other side chains in the final non-peptide combinatorial libraries (Step 3).

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In order to model the candidate M₁ functional groups in this conserved catalytic region of the PKA active site, they were built onto the P 0 Ala position in the PKA ternary structure using the SYBYL molecular modeling package (Tripos) on a Silicone Graphics workstation as indicated in Figure 3.

- 5 A crystal structure of PKA with MgATP and an inhibitor bound in a more “open” conformation was not available, so initial modeling studies were carried out on the MgADP bound form of PKA derived from the ternary complex illustrated in Figure 2 by simply deleting the ATP γ -phosphate. Initial modeling studies were used to provide qualitative guidance for identifying interesting potential M₁ functional
- 10 groups for the protein kinase family before synthesis and testing. The most advanced computational algorithms for quantitatively predicting the free energy of binding, such as Free Energy Perturbation methods, are computationally intensive methods which are not practical at this point in time for routine use by the non-specialist. Even the most advanced methods can be inaccurate due to difficulties in sampling,
- 15 inadequacies in the molecular mechanics force fields/parameters, and an incomplete understanding of electrostatics in water (Ajay & Murcko, 1995). Less rigorous (and easier to use) computational methods tend to be unreliable in making quantitative predictions of binding affinities, especially when dealing with multiple polar and ionic interactions such as those involved in M₁ binding.
- 20 In order to allow molecular mechanics calculations to be done with the Silicone Graphics workstation in a reasonable amount of time, two layers of residues were carved out from the PKA ternary structure which are surrounding the PKA active site, along with the peptide inhibitor and Mg₂ADP. The M₁ functional groups were then appended to the P 0 Ala side chain and the entire PKA active
- 25 site:Mg₂ADP:modified peptide inhibitor complex was then subjected to 300 iterations of molecular mechanics minimization using the Tripos force field with a distance dependent dielectric constant after assigning appropriate formal charges and calculating Gasteiger Marsili point charges using SYBYL. Setting the maximum number of iterations at 300 was sufficient to remove any serious strain in the
- 30 complexes and yet not allow the overall structure to “drift” significantly from the starting x-ray structure if convergence is not reached. These minimized complexes were then visually evaluated to determine if the appended individual M₁ functional

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groups were able to engage in favorable interactions with the conserved catalytic residues and/or Mg_2ADP . This visual evaluation involved, among other standard interaction evaluations, measuring atom-atom distances to determine if hydrogen bonds and ionic interactions were being favorably formed.

5 Favorable intermolecular interactions between an individual M_1 functionality and the conserved catalytic residues or Mg_2ADP does not necessarily mean enhanced binding affinity will be observed for the new inhibitor. Unfavorable desolvation of both the polar M_1 functionality and the polar PKA active site residues (as well as complex entropy effects) are not included in this analysis and may reduce the net
10 binding affinity to the point that the modified inhibitor may even be less potent than the corresponding P 0 Ala inhibitor, even though the appended M_1 functionality is interacting with the conserved catalytic residues and/or $MgADP$ (or $MgATP$) as intended. Even in cases where this desolvation penalty results in no net increase in binding affinity, these M_1 functional groups are still useful as an orienting groups for
15 correctly positioning the non-peptide inhibitor analogs in the protein kinase active site. Positioning these polar functional groups elsewhere within the active site (assuming they are tethered so as not to be able to extend into bulk solvent while the scaffold is favorably bound in the active site) is likely to result in a reduced binding affinity because they were specifically designed and selected based upon their
20 demonstrated ability (while appropriately tethered to pentapeptide scaffolds) to be accepted adjacent to the conserved catalytic residues and $MgADP/MgATP$. If a particular M_1 functionality does not correctly position a non-peptide scaffold in Step 1 then attempts to improve the potency by rationally appending initial specificity elements in Step 2 would likely fail.

25 None of the literature protein kinase assay procedures contain added ADP. A typical PKA literature assay procedure (Glass et al., 1989) was modified by adding 10% as much ADP as the ATP concentration used to reflect the natural 1/10 ratio in the cell. This protein kinase assay is hereinafter referred to as the "Literature Mimetic" assay. It has been used for PKA as well as the Src. An examination of the
30 literature, and commercially available protein kinase assays, showed that there is poor consistency from lab to lab and company to company and that all of these assays use physical chemical conditions which differ considerably from those known to exist

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inside cells. Since inhibition of intracellular protein kinases is the ultimate goal for drug discovery, new protein kinase assays have been developed which come much closer to mimicking the overall cytosolic physical chemical conditions known to exist inside cells. The development of these "Cellular Mimetic" protein kinase assays, is
5 described herein, along with a novel method for determining which form of a protein kinase a given inhibitor binds best to (the STAIRe method). Data was collected correlating the activity of the new non-peptide Src inhibitors in the Cellular Mimetic assay with that obtained in the LA25 Src transformed cell line (see below).

When these two assay conditions were applied to some of the pentapeptide-
10 based PKA inhibitors, which were designed as illustrated in Figure 3, the results shown in Table I were obtained. The same assay conditions were also applied to the analogously designed pentapeptide-based Src inhibitors and obtained the results shown in Table II.

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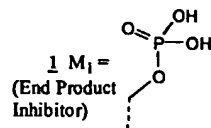
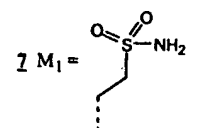
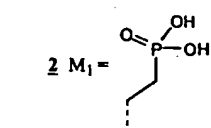
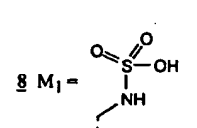
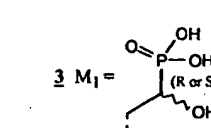
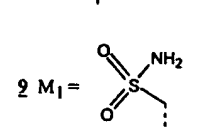
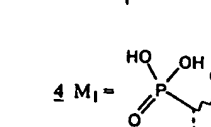
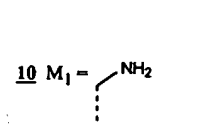
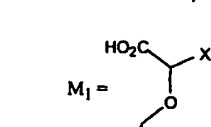
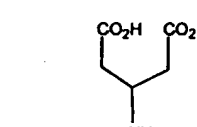
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TABLE I
INITIAL M₁ SCREENING RESULTS WHILE APPENDED
TO THE PKA PENTAPEPTIDE SCAFFOLD

----- = Attachment Point

$\text{Ac-Arg-Arg-Gly-NH-} \overset{\text{M}_1}{\text{CH}} \text{-C(=O)-Ile-NH}_2$

	<u>K_i (μM), (Conditions*)</u>		<u>K_i (μM), (Conditions*)</u>
	* L=Literature Mimetic C=Cellular Mimetic		* L=Literature Mimetic C=Cellular Mimetic
$\text{1 M}_1 =$  (End Product Inhibitor)	5 (L) 542 (C) \rightarrow 108 X	$\text{7 M}_1 =$ 	300 (L) 2400 (C) \rightarrow 8 X
$\text{2 M}_1 =$ 	76 (L) NT (C)	$\text{8 M}_1 =$ 	0.16 (L) 5 (C) \rightarrow 31 X
$\text{3 M}_1 =$  (R or S)	18 (L)-Diastereomer A 72 (L)-Diastereomer B NT (C)	$\text{9 M}_1 =$ 	250 (L) 2100 (C) \rightarrow 8 X
$\text{4 M}_1 =$  (R or S)	4 (L)-Diastereomer A 20 (L)-Diastereomer B 171 (C)-Diastereomer A 1510 (C)-Diastereomer B \rightarrow 43 X	$\text{10 M}_1 =$ 	38 (L) 115 (C) \rightarrow 3 X
$\text{M}_1 =$  X	5 X = H 28 (L) 780 (C) \rightarrow 29 X	$\text{11 M}_1 =$ 	45 (L) NT (C)
$\text{6 X = CO}_2\text{H}$	6 (L) 450 (C) \rightarrow 75 X		

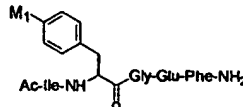
The structure identified in Table I as Ac-Arg-Arg-Gly-Ala bonded to M₁-Ile-NH₂ is
 SEQ. ID. No. 2.

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
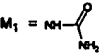

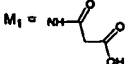

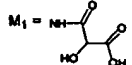

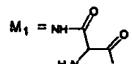
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TABLE II
INITIAL M₁ SCREENING RESULTS WHILE
APPENDED TO THE SRC PENTAPEPTIDE SCAFFOLD



Ac-Ile-NH-CH(CH₂-C₆H₄-M₁)-CO-Gly-Glu-Phe-NH₂

% Inhibition of 2 mM RR-src phosphorylation by src

Inhibitor (1 mM)	Assay Conditions		Inhibitor (1 mM)	Literature Mimetic	Cellular Mimetic
	Literature Mimetic	Cellular Mimetic			
12 M ₁ = 	36	0	16 M ₁ = 	60	8
13 M ₁ = 	51	0	17 M ₁ = 	20	28
14 M ₁ = 	83	88	18 M ₁ = 	64	5
15 M ₁ = 	68	59	19 M ₁ = 	24	0

The structure identified in Table II as Ac-Ile-Tyr bonded to M₁-Gly-Glu-Phe-NH₂ is SEQ. ID. No. 3.

The standard pentapeptide sequence chosen for the majority of PKA inhibitors in Table I was derived from the pseudosubstrate sequence of the peptide inhibitor which was bound to PKA, when the crystal structure illustrated in Figure 1 was solved. The standard pentapeptide sequence used for Src in Table II, Ac-Ile-Xaa-Gly-Glu-Phe-NH₂ (SEQ. ID. No. 3), was described in Nair, Kim et al., 1995. Some of the chemistry used to prepare the PKA inhibitors is described in Nair, Lee & Hangauer 1995. The synthetic methodology used to develop a number of the Src inhibitors is described in Lai et al., 1998.

The collective results in Tables I and II show that both the serine kinase PKA and the PTK Src can accommodate a variety of large polar M₁ functional groups at the P 0 phosphorylation position. Furthermore, using the STAIR methodology (see Choi et al. 1996), the sulfamic acid inhibitor **8**, and related inhibitors, were shown to actually bind best when MgATP (not MgADP or no nucleotide) is also bound. This was a somewhat surprising result since these inhibitors are analogs of the "end product inhibitors" **1** and **12** which must bind simultaneously with MgADP just following phosphate transfer in the generally accepted reaction mechanism for protein kinases.

These results also demonstrate that both PKA and Src can show a large difference in binding affinity for structurally very similar inhibitors. For example, the

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sulfamic acid PKA inhibitor 8 (Table I) has a K_i of 0.16 μ M under Literature Mimetic assay conditions (L) whereas the isosteric sulfonamide 7 is 1,875 X less potent (K_i = 300 μ M). The sulfamic acid inhibitor 8 is also isosteric with the end product phosphate inhibitor 1 yet it binds much more tightly under both Literature Mimetic
5 assay conditions (31 X) and Cellular Mimetic (C) assay conditions (108 X). The beneficial effect of an oxygen atom positioned analogously to that in the substrate Ser is illustrated by comparison of phosphonate 2 to phosphate 1 and also ether 6 to phosphate 1. This oxygen atom can also be positioned as a serine-like OH side chain and enhance binding (compare 2 to 3A and 4A) wherein the closer serine mimic 4A is
10 the more active. The difference in activity of the diastomeric inhibitors 3A or B and 4A or B suggests a specific interaction with the active site catalytic residue Asp-166 may in fact be occurring as intended in the M_1 design (Figure 3).

The Src inhibition results (Table II) show that the end product inhibitor 12 drops in activity upon going from Literature Mimetic assay conditions to the higher
15 ionic strength Cellular Mimetic assay conditions, analogous to the PKA end product inhibitor 1. However, whereas all of the PKA inhibitors with polar M_1 functional groups were less active under Cellular Mimetic assay conditions, three of the Src inhibitors 14, 15, and 17 held their activity under these higher ionic strength assay conditions. Also, the hydroxyphosphonate Src inhibitor 13 (a mixture of the R and S
20 diastereomers) is analogous to the PKA inhibitor 3A and both are roughly in the same activity range as their corresponding end product inhibitors, 12 and 1 respectively, under Literature Mimetic assay conditions. Shortening the side chain length in the phosphonate Src inhibitor 13 by one carbon atom (and necessarily removing the attached OH at the same time) to give 14 improved the activity (analogous to the PKA
25 inhibitor comparison 3 to 4) and, more importantly, resulted in equivalent activity under Cellular Mimetic assay conditions. The Src results with 16-19 (particularly 17, see later for an analogous α -tricarboxyl acid M_1 analog appended to non-peptide Src inhibitors) also suggests that similar amides may be useful M_1 functional groups to explore with non-peptide Src inhibitors.

30 Non-peptide Src inhibitors are preferred to peptide scaffold based compounds, partly because some of these inhibitors have a dual effect on Src. For example, phosphonate inhibitor 14 not only inhibits Src by competitively binding in the active

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site but it also activates Src by binding to the SH₂ site thereby releasing the intramolecular autoinhibition mechanism (Xu et al., 1997). This opposing effect gives an unusual IC₅₀ curve for **14**, wherein at low inhibitor concentrations Src is stimulated (to a maximum of 70%) in a smooth dose-response fashion (due to initial tighter SH₂ binding) followed by a typical IC₅₀ inhibition curve at higher inhibitor concentrations (due to lower affinity blockade of the active site). This opposing activation effect of the pentapeptide inhibitors makes them appear to be less potent active site inhibitors than they in fact are, and makes it difficult to accurately rank M₁ groups while appended to this pentapeptide scaffold. However, the better M₁ groups identified with the Src pentapeptide scaffold must still be accommodated in the catalytic region of the active site and hence are useful orienting groups for the ongoing non-peptide Src inhibitor studies as intended. Since PKA does not have an SH₂ domain, this complication is not a factor in interpreting the PKA pentapeptide inhibitor M₁ testing data.

The results in Tables I and II also show how much effect the assay conditions can have on both inhibitor potencies and the rank order of activity. For example, as shown in Table I, switching from the Literature Mimetic (L) assay conditions to the Cellular Mimetic (C) assay conditions can change the potency from as little as 3-fold (inhibitor **10**) to as much as 108-fold (inhibitor **1**). Also, whereas inhibitor **10** is less potent than **1** under Literature Mimetic conditions, it is more potent under Cellular Mimetic conditions. The Src inhibitor data presented in Table II show that many of the inhibitors lose their potency upon going from Literature Mimetic assay conditions to Cellular Mimetic assay conditions. The rank order of potency against Src is also sensitive to the assay conditions. Whereas inhibitor **18** is more potent than inhibitor **17** under Literature Mimetic conditions, the opposite is true under Cellular Mimetic conditions. Since activity within cells is the goal, the Cellular Mimetic Src assay was selected as the standard assay for testing potential non-peptide Src inhibitors. Activity within the Cellular Mimetic assay is a necessary, but not sufficient, condition for activity within cells. As will be described later, the Cellular Mimetic Src assay will be followed up with cell culture assays wherein cell penetration, metabolism, and binding to other cellular components are also factors in the measured potency.

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The next class of M_1 functionality which was explored was the boronic acid group. This functional group is an intriguing candidate for M_1 for a number of reasons: 1) It can exist in a non-ionic state so that it should not prevent passive absorption of non-peptide inhibitors across cell membranes. 2) The planar, trigonal, boron acids might form reversible tetrahedral covalent borate complexes (a well known property of boronic acids, see Loomis & Durst, 1992) through their vacant 2p orbitals with anions present in the protein kinase active site, such as the catalytic Asp carboxyl group, or the ATP/ADP terminal phosphate oxygens. This ability to form borate complexes with active site nucleophiles has been extensively utilized to develop slow binding inhibitors of serine proteases (e.g. see Kettner & Shenvi, 1984), wherein the nucleophilic serine OH forms a covalent bond with the vacant 2p orbital in the boronic acid resulting in a tetrahedral borate complex (e.g. see Skordalakes et al., 1997). Also, an intramolecular complex of a boronic acid with a urea NH_2 was used to prepare transition state analogs inhibitors of dihydroorotase (Kinder et al., 1990). 3) Boronic acids act as Lewis acids and are converted to tetrahedral hydrates in water by forming borate complexes with water or hydroxide ions. Therefore, it is also possible that these boronic acid hydrates may function as phosphate mimics and M_1 modules as proposed in Figure 2. This hydration property was utilized by Baggio et al. (1997) wherein a hydrated boronic acid functioned as a transition state analog inhibitor functionality for arginase. These researchers evaluated the inhibited complex by x-ray and showed that the hydrated boronic acid functionality formed two hydrogen bonds with the active site catalytic Glu-277 carboxyl side chain and one of the other hydrated boronic acid OH's interacted with two catalytic Mn^{2+} 's in the active site. These binding interactions are closely analogous to those proposed in protein kinase active sites, i.e. H-bonds to the catalytic Asp side chain carboxyl group and interactions with the active site Mg^{2+} 's (see Figures 2 and 4). The use of boronic acids for protein kinase inhibitors has not been explored previously.

In the area of pentapeptide-based PKA inhibitors, the boronic acid functionality has been prepared and tested as a potential M_1 module utilizing the four inhibitors 21-24 shown in Table III (see Hsiao & Hangauer, 1998, for some of the chemistry used to prepare these compounds).

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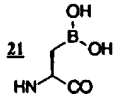
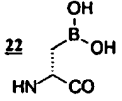
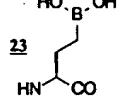
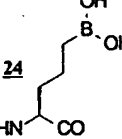
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TABLE III

PKA INHIBITION RESULTS WITH BORONIC ACID-CONTAINING PEPTIDE INHIBITORS

5

Ac-RRGXI-NH ₂ , X =	IC ₅₀ μM (cond. L, 0 h preincubation)	IC ₅₀ μM (cond. L, 4 h preincubation)	IC ₅₀ μM (cond. C, 0 h preincubation)	IC ₅₀ μM (cond. C, 4 h preincubation)
<u>20</u> Ala	278 (K _i = 9 μM)	417	41 (K _i = 25 μM)	50
<u>21</u> 	249	* 500 μM 34% inh	764	* 2000 μM 19% sti
<u>22</u> 	81	* 65	* 1753	* 2000 μM 71% sti
<u>23</u> 	398	133	2000 μM 16% inh	* 2000 μM 5% inh
<u>24</u> 	1000 μM 33% inh	1000 μM 44% inh	2000 μM 6% sti	1734 μM

* Very distorted IC₅₀ curve: Suggests Inhibitor is also a substrate.

L = Literature Mimetic Assay Conditions.

C = Cellular Mimetic Assay Conditions.

Inh = Inhibition.

Sti = Stimulation.

10 The structure identified in Table III as Ac-RRGXI-NH₂ is SEQ. ID. No. 4.

While testing these boronic acid-containing PKA inhibitors, the corresponding pentapeptide pseudosubstrate inhibitor 20 was included as an internal control while investigating time-dependent inhibition as shown in Table III. Under Literature Mimetic assay conditions, and no preincubation, the initial results suggested that the

15 shortest chain L-amino acid 21 was binding with the same affinity as the pseudosubstrate inhibitor 20 (i.e. K_i ca. 9 μM). As this side chain was increased in length (to 23 and then 24) binding affinity appeared to decrease. When the stereochemistry of the unnatural amino acid was inverted from L in 21 to D in 22, binding affinity appeared to increase 3-fold. This improvement in binding may occur

20 as a result that the boronic acid OH in 21 is positioned at the same chain length as L-homoserine whereas the natural substrate, L-serine, has a one carbon shorter side chain. Modeling results with the PKA ternary structure indicated that the boronic acid

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OH can be retracted back somewhat by inverting the α -carbon stereochemistry from L in 21 to D in 22 and then repositioning the side chain to more closely mimic the positioning of the natural substrate L-serine OH adjacent to the catalytic residues (Asp-166 and Arg-168). The modeling results were subsequently supported by the
5 finding that, upon incubation of PKA with these inhibitors for up to four hours without adding the competing peptide substrate (Kemptamide: LRRASLG-NH₂ (SEQ. ID. No. 5)), both 21 and 22 function as substrates with the D-diastereomer 22 being phosphorylated faster.

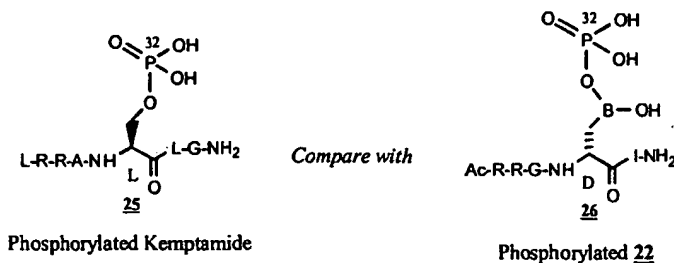
The fact that these boronic acid inhibitors are also substrates, became much
10 more obvious by the greatly distorted IC₅₀ curves obtained under the Cellular Mimetic conditions, both with and without preincubation (both PKA and Src are more active enzymes under the Cellular Mimetic conditions than under Literature Mimetic conditions). In the assay used to obtain these results, the P³² phosphorylated Kemptamide product (25 generated from γ -P³² ATP) was isolated at the end of the
15 substrate incubation period by binding to phosphocellulose filter paper via the three cationic groups (two Arg's and the N-terminus) and the level of phosphorylated product isolated on the paper is then measured by liquid scintillation counting (cpm's). The boronic acid inhibitors 21-24 have two Arg's in their sequence also and therefore will bind to the phosphocellulose paper in addition to Kemptamide
20 (although not as consistently or completely due to one less positive charge). Consequently, when analyzed as inhibitors, the amount of phosphorylated Kemptamide produced was not only counted, but also the amount of phosphorylated inhibitor simultaneously produced (e.g. see 26 below). The net result is that distorted IC₅₀ curves are obtained which show net "stimulation" at higher inhibitor
25 concentrations in some cases. The D diastereomer 22 gives the greatest apparent "stimulation" (71%) when preincubated with PKA for four hours under Cellular Mimetic conditions followed by the L diastereomer 21 (19%) and then the one carbon homolog 23 (5%), indicating all three are substrates for PKA (Table III). The underlying substrate behavior of these "inhibitors" makes an accurate measurement of
30 their inhibition potency impossible with the current assay. However, it does appear from the data that homologating the boronic acid functionality out with only CH₂

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groups (homologations with boronic acid non-peptide Src inhibitors may also be carried out) decreases the binding affinity and ability to function as a substrate.



5

Phosphorylated Kemptamide is SEQ. ID. No. 6. Phosphorylated 22 is SEQ. ID. No. 4. The boronic acid "inhibitors" 21 and 22 were shown to be substrates for PKA by running the same assay, but without adding Kemptamide, and stopping the reaction at various time points as shown in Figure 4. The graphs show their

10 respective rates and levels of phosphorylation with the typical loss of initial velocity kinetics with time (due to substrate depletion and end product inhibition), analogous to a standard L-Ser substrate such as Kemptamide. The comparison of 21 to 22 shown was done in the same assay run, at identical boronic acid substrate concentrations, and with identical Cellular Mimetic assay solutions so that the cpm's

15 could be directly compared. The graphs show that initial velocity conditions were lost within one hour for D isomer 22 whereas the linearity appears to have been lost somewhat slower with the L isomer 21 suggesting a slower consumption of starting material. That the boronic acid moiety would be phosphorylated by PKA was surprising, but it is even more surprising that the phosphonic-boronic acid mixed

20 anhydride produced (e.g. 26) was stable enough to survive the pH 7.2/37°C assay incubation and then be isolated by binding to phosphocellulose paper after acid quenching of the reaction with 10% TCA and washing the phosphocellulose paper with 25 mM phosphoric acid (3X). An STN substructure search was run on mixed anhydrides of phosphoric and boronic acids and found only three references to

25 experiments and theoretical calculations for the analogous putative (but not proven) anhydride formed from boric acid and phosphoric acid as a solid surface impregnated catalyst for the partial oxidation of ethane to acetaldehyde at 823 °K (Zhanpeisov & Otsuka, 1992, Otsuka et al., 1992, Murakami et al., 1990). However, this highly

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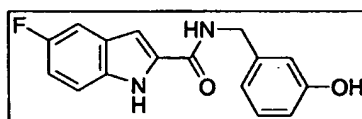
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unusual anhydride has never before been synthesized free of a solid surface, isolated, or characterized. Thus, this is a novel enzymatic reaction and chemical entity with interesting possibilities for protein kinase inhibitor designs.

The next class of M_1 functionality which was explored was the halogen group.

- 5 This functional group is an intriguing candidate for M_1 for a number of reasons: 1) it is a good hydrogen bond acceptor; and 2) it reduces the rate of metabolism, leading to *in vivo* benefits.

The halogen functionality has been prepared and tested as a potential M_1 module utilizing the inhibitor shown below (see Example 1, for the chemistry used to
10 prepare this compound).



This inhibitor was tested for Src inhibition using the assay procedure set forth in Example 1. The results obtained are shown in Table VII, which indicates an IC_{50} of 40 μM for the above inhibitor (1a in Table VII). This inhibitor includes a non-
15 peptide scaffold (indole) which was chosen based on the screening method described below.

The Src and PKA pentapeptide scaffold tethered M_1 evaluations described above have resulted in identifying a variety of orienting M_1 groups which could be used for screening potential non-peptide scaffolds as indicated in Step 1 (Figure 1).
20 The boronic acid (from 22), the phosphonate (from 14), and the sulfamic acid (from 8) were chosen from the menu of potential M_1 's for the Src non-peptide scaffold screening. Among these choices, the boronic acid M_1 group has proven effective for Step 1 screening of non-peptide scaffolds.

The most useful crystal structures available for the design of non-peptide Src
25 inhibitors, which do not compete with ATP, are the native Src structure and the IRTK:peptide:AMP-PNP ternary structure. For all of the modeling studies discussed below, the SYBYL molecular modeling software package is used on a Silicone Graphics Workstation.

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Since the Src and IRTK structures are only used as qualitative guides in designing the non-peptide scaffolds and combinatorial libraries, the active sites along with two layers of surrounding residues were carved out from the native Src and IRTK ternary structures, analogous to the previous PKA modeling studies. The IRTK:peptide:AMP-PNP ternary structure active site region was used as the template structure to guide the building of the Src residue sequence 424-418 back onto the Src structure using the comparative homology modeling technique (see Hutchins & Greer, 1991). These residues were disordered in the native Src crystal structure and therefore not visible by x-ray. They were reintroduced because they help form the P+1 to P+3 binding sites for peptide substrates which are important for some of the modeling studies. The analogous residues in the IRTK ternary structure are seen by x-ray and directly interact with the bound peptide substrate. In fact, it is probably the presence of the bound peptide substrate which induces order in the positioning of this sequence so that it is visible by x-ray. The Src pentapeptide substrate Ac-Ile-Tyr-Gly-Glu-Phe-NH₂ (SEQ. ID. No. 1) (Nair et al., 1995) was then docked into the Src active site again using the IRTK ternary structure as a template. Small adjustments were then manually made to partially clean up this complex, all of the hydrogen atoms were added, appropriate formal and partial charges (calculated via the Gasteiger Marsili method) were added, and then the entire complex was subjected to 300 iterations of molecular mechanics minimization using the Tripos force field, analogous to the previous PKA modeling procedure. A schematic representation of this modeled complex is given in Figure 5. Any inaccuracies in this Src:peptide and the Src:inhibitor models are accommodated by experimentally evaluating a range of side chains, the number and diversity of which is scaled roughly to the level of uncertainty for the structure of their particular binding region in the Src model active site (see later), in a combinatorial fashion.

As shown in Figure 5 the residues 424-418 built back into the Src interact with the P+1 to P+3 substrate residues, Gly-Glu-Phe-NH₂ respectively, through beta sheet type hydrogen bonding interactions with the substrate main chain (analogous to the IRTK peptide substrate). Lys 423 engages in two important interactions: 1) the β and γ CH₂'s fold over the top of the P O Tyr phenyl ring engaging in a hydrophobic binding interaction and then 2) the remaining CH₂-CH₂-NH₃⁺ of this side chain

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extends away to form a salt bridge with the P+2 Glu side chain as indicated. The rest of the P 0 Tyr hydrophobic binding pocket is formed by Pro 425 under the phenyl ring and part of the Cys 277 side chain above the phenyl ring. Using a large combinatorial peptide Src substrate library, Songyang et al. (1995) found that the most commonly
5 chosen side chain for the P+1 position was Gly followed by Glu. The present model indicates that a P+1 Glu side chain may form a salt bridge with nearby Arg 469 as indicated in Figure 5. Previously, researchers found that only Glu was chosen for the P+2 position and the present model indicates that this side chain forms a salt bridge with the Lys 423 side chain. At the P+3 position Phe was very strongly preferred and
10 the model indicates that this side chain forms a stacking interaction with the Phe 424 side chain. At the P-1 position Songyang et al. found that Ile was the most preferred residue followed by Val and then Leu. The model shows a hydrophobic pocket for binding the P-1 side chain formed mainly by Trp 428, Ala 390 and Leu 347. One might expect that the P 0 Tyr side main chain will strongly interact (though hydrogen
15 bonding) with the active site in a catalytically competent complex because enzymes often form more critical interactions in this region close to where the reaction will be occurring. The IRTK ternary complex does not show a good hydrogen bond to either the P 0 Tyr NH or carbonyl. The nearest candidate residue for this interaction in the IRTK structure is Asn 1215 wherein the side chain NH₂ is 3.71 Å from the Tyr
20 carbonyl oxygen. When the IRTK ternary structure is overlayed onto the Src native structure, using the four residues mentioned in the Background and Significance section, Asn 468 from the Src structure was found to be positioned very close to the analogous IRTK Asn 1215. This suggests that this conserved residue is performing an important role and might move a little closer (i.e. about 1 Å) to the substrate P 0
25 NH and carbonyl in a catalytically active complex and form the hydrogen bonding interactions indicated in Figure 5. Finally, the catalytic Arg 388 and Asp 386 are correctly positioned in the Src model to catalyze the transfer of the γ-phosphate from ATP to the Tyr OH.

The Src:peptide substrate complex can now be used to model potential non-
30 peptide scaffolds and determine preferred substitution positions for the specificity elements, all with an appropriately attached M₁ functionality, before choosing new scaffolds to experimentally evaluate. The IRTK:peptide:AMP-PNP ternary structure

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can also be used to model these potential scaffolds and preferred substitution positions. These scaffolds have broad utility for the development of selective PTK inhibitors by further developing them with appropriate specificity elements following the strategy outlined in Figure 1.

5 The first non-peptide scaffold evaluated with this Src:peptide substrate model was the naphthalene scaffold. This is the first use of bicyclic aromatic scaffolds for non-peptide PTK inhibitors, which do not compete with ATP. The naphthalene scaffold's utility for this purpose was demonstrated by developing a non-peptide inhibitor of the IRTK and EGF receptor PTK (Saperstein et al., 1989). The IRTK
10 ternary complexes were subsequently used to adapt this scaffold for Src inhibition (see Marsilje et al., 2000). The naphthalene scaffold was docked into the Src active site by first carrying out a least squares fitting of atoms *a-d* onto the peptide substrate as indicated in Figure 6. In this way the naphthalene scaffold is related to the peptide
15 substrate by the cyclization shown by the arrow in Figure 6 and an appended OH as a substitute for the substrate Tyr NH. This is essentially the same process used to dock this scaffold into the IRTK structure as described in Marsilje 2000. The peptide
20 substrate was then deleted from the active site, various M₁ functional groups and specificity elements S₂ and S₃ were then added to the scaffold as indicated and the complexes were then individually minimized for 300 iterations. This same process
20 was also used to design the isoquinoline and indole scaffolds whose binding modes are indicated in Figure 7.

 In all of these modeled complexes, selectivity element S₂ consists of various hydrophobic side chains which can bind in the same pocket as the substrate P-1 Ile side chain and selectivity element S₃ consists of various molecular fragments which
25 can bind in the P+1 to P+3 region of the peptide substrate binding sites (Figure 5). Since the active site region where M₁ binds is highly conserved among all of the protein kinases, the small menu of M₁ functional groups previously identified using peptide scaffolds served as the initial M₁ groups for attachment to the scaffolds at the indicated positions. Of the two selectivity elements binding sites, the structure of the
30 hydrophobic binding cavity for S₂ is known with greater confidence in the Src model than is the P+1 to P+3 binding region for S₃. This is because the S₃ binding site was constructed partially by comparative homology modeling whereas the S₂ site is

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largely unchanged from the structure determined by x-ray for native Src. In view of these varied levels of confidence in the modeled binding sites for M₁, S₂ and S₃, the combinatorial library diversity is scaled such that the greatest variety and number of side chains in the combinatorial libraries are at the S₃ site followed by the S₂ site and then M₁.

The Src results using M₁ functional groups to experimentally identify promising non-peptide scaffolds are listed in Table IV.

TABLE IV
INITIAL STEP 1 RESULTS
% SRC INHIBITION IN CELLULAR MIMETIC ASSAY

Inhibitor	% Inhibition of 2 mM RR-src at Inhibitor Concentration ()		Inhibitor	% Inhibition of 2 mM RR-src at Inhibitor Concentration ()
	---	Attaching bond.		
	59 (1 mM) 13 (100 μM) IC ₅₀ =950 μM K _i =554 μM	NON-ATP COMPETITIVE		10 (100 μM)
	31 (1 mM) IC ₅₀ =1.6 mM K _i =963 μM	NON-ATP COMPETITIVE		13 (500 μM)
	0 (1 mM)			62 (500 μM)
	14 (1 mM)			11 (500 μM)
	0 (100 μM)			13 (100 μM)
	0 (100 μM)			14 (100 μM)
	1 (1 mM)			
	0 (100 μM)			

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The data in Table IV allows a number of conclusions to be drawn: 1) Low, but measurable, inhibition potency can be obtained with an appropriate M₁ group attached to a scaffold (e.g. 27 and 38). 2) 1 mM inhibitor concentrations for this type of screening is higher than desirable but 100 μ M is too low. Screening of scaffolds bearing an M₁ group would optimally be conducted at 500 μ M. 3) The boronic acid, sulfamic acid, and phosphonic acid M₁ functional groups, which had been identified using the PKA pentapeptide scaffold (22, Table III and 8, Table I) or the Src pentapeptide scaffold (14, Table II), respectively, give measurable activity when placed at the 2 position of the naphthalene ring (27, 28, and 30, respectively), the preferred position for M₁ identified in the model naphthalene inhibitor:Src complex (Figure 6). Moving the boronic acid or phosphonic acid M₁ groups to the 1 position (32 or 33) reduced activity. 4) The related M₁ sulfonamide functionality, which was poor on the PKA pentapeptide scaffold (7 & 9, Table I) is also poor when appended to the 2 (31) or 1 (34) position of the naphthalene scaffold. The sulfonic acid analog at the naphthalene 2 position (29) is completely inactive, even at 1mM. 5) The naphthalene scaffold can be replaced with a benzofuran (35) or a benzothiophene (36) scaffold without a noticeable reduction in activity when the boronic acid M₁ group is positioned analogous to the 2 position on a naphthalene. 6) The boronic acid M₁ group also provides active compounds when appended to the isoquinoline (37) or indole (38) scaffolds at the positions indicated by modeling results (Figure 7). However, the indole scaffold is clearly favored over the isoquinoline scaffold suggesting that a hydrogen bond donating ability to Asn 468 (see Figure 7) is important for higher activity (this would require the protonated isoquinoline which is disfavored by the adjacent electron withdrawing ester group). This conclusion is also supported by considering that a peptide substrate may position a hydrogen bond donating peptide bond NH at a similar position (Figure 6) and by finding that an equivalently positioned phenolic OH (Figure 6) improves potency (phenolic OH's are much better H-bond donors than acceptors). 8) When directly compared to other M₁ groups, the boronic acid group is superior (e.g. 27 vs. 28-31, 38 vs. 39). 9) A biphenyl scaffold modeled into the Src and IRTK active sites and found promising

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binding modes for this scaffold. Combinatorial libraries were developed with the biphenyl scaffold (see Pavia et al., 1996), and the modeling results were encouraging. Therefore, the para (40) and meta (41) isomers were evaluated with the boronic acid M₁ group. Both biphenyl compounds showed potency equivalent to the best
5 naphthalene boronic acid (27) and therefore provide another scaffold geometry (the two phenyl rings are not planar) for further evaluation and development.

Since the bare scaffolds, with only an M₁ group appended, often have low binding affinity, the IC₅₀'s and K_i's for the 2-naphthalene boronic acid and sulfamic acid inhibitors were determined to ensure that a typical dose/response IC₅₀ curve is
10 obtained. This analysis provided the typical shape dose/response curves seen with more potent inhibitors. The IC₅₀'s and K_i's of these simple inhibitors also confirmed that the boronic acid inhibitor 27 is more potent than the sulfamic acid analog 28 and has a K_i of about 554 μM.

The next issue addressed with these simple inhibitors before proceeding to
15 elaborate them further was their mode of inhibition, specifically whether they are ATP-competitive inhibitors. In the case of the naphthalene inhibitors 27 and 28, their IC₅₀'s were monitored as the ATP concentration was increased in three steps up to 1 mM. As a comparison, the IC₅₀ of the pentapeptide phosphonic acid Src inhibitor 14 (Table II) was also monitored. If any of these inhibitors were competing with ATP,
20 then their IC₅₀'s should have increased proportionally with the ATP concentration (i.e. the dashed line). As shown, the IC₅₀'s for all three inhibitors remained essentially constant as the ATP concentration was increased demonstrating that they are not ATP-competitive inhibitors. A very similar, but much less costly (commercial Src is expensive), analysis was conducted with the indole boronic acid inhibitor 38.
25 In this case, the % inhibition was monitored with 38 at a constant 500 μM inhibitor concentration but with increasing ATP concentrations of 200, 500 and 1,000 μM. Once again the inhibitor potency was not reduced by the increasing ATP concentration demonstrating that 38 is also non-ATP competitive.

The initial results obtained in Step 1 suggests that it is possible to identify
30 promising scaffolds for further elaboration with this procedure. The biggest uncertainty with Step 1 is that some of the scaffolds identified in this way might not be binding in the fashion suggested by the prior modeling evaluations. This is

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essentially a "false positive" problem. These "false positives" will likely fail in Step 2, when they are evaluated for improved binding using the modeled complexes as a guide. Some false positive results can be accepted in Step 1 because the bare scaffolds with only the M_1 group attached are easily obtained. For further inhibitor development, one may return to Step 1 each time new scaffolds are needed to carry through Steps 2 and 3. The best M_1 generated can be used each time Step 1 is repeated. Currently, the boronic acid M_1 group has been used since it has a proven ability to give measurable activity with bare scaffolds. Also the boronic acid M_1 group offers multiple interesting possibilities for covalent and non-covalent interactions with the conserved catalytic residues since it can: 1) hydrate, 2) form borate complexes with electron rich active site atoms, and/or 3) be phosphorylated and then react with active site nucleophiles or engage in additional non-covalent interactions. From the data in Table IV, the naphthalene and indole scaffolds were chosen as M_2 for the first efforts in Step 2 (the biphenyl scaffold is also a preferred scaffold). It is also worth mentioning that naphthylalanine and analogs can be successfully substituted for the P 0 tyrosine in Src peptide substrates (e.g. see Alfaro-Lopez et al., 1998) further supporting the notion that naphthalene and related scaffolds can bind at the P 0 site.

In comparing the naphthalene vs. indole scaffold results with a boronic acid M_1 group (i.e. 27 vs. 38, Table IV) the indole hydrogen bond donating NH and/or the adjacent ester group appeared to be the reason for the enhanced potency. Consequently, for Step 2 one of the first attempts was to add a hydroxyl group and an amide (with S_2) to the naphthalene scaffold at the adjacent positions suggested by the modeling results (Figure 6). For the indole scaffold one priority was to prepare some amide analogs to see if potency can be increased with the S_2 specificity element (Figure 7). In order to facilitate the synthesis of these initial analogs, an OH was temporarily substituted for the boronic acid M_1 group. The OH group is also known to interact with the catalytic residues, as required for an M_1 group, because it is the natural substrate M_1 whose phosphorylation rate is accelerated by interactions with the catalytic residues. The results obtained for some of the initial analogs are given in Table V along with a side by side comparison, in the Cellular Mimetic Src assay, to

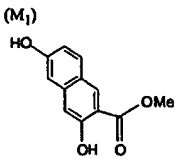
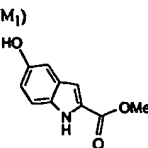
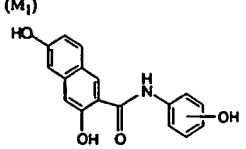
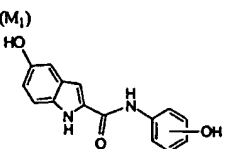
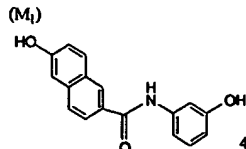
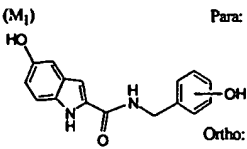
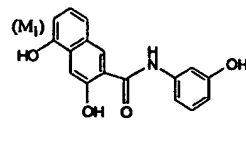
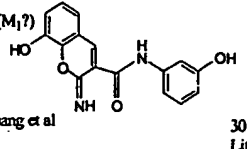
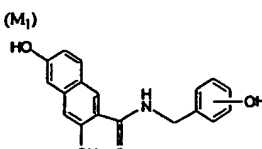
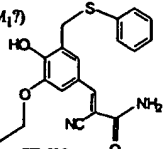
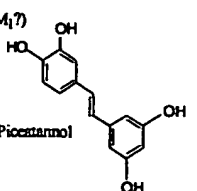
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two literature Src inhibitors 50 and 51 which are reported be non-ATP competitive. Some of these results and additional analogs are described in Marsilje 2000.

TABLE V
INITIAL STEP 2 RESULTS
% SRC INHIBITION IN CELLULAR MIMETIC ASSAY

Inhibitor	% Inhibition of 2 mM RR-src at Inhibitor Concentration ()	Inhibitor	% Inhibition of 2 mM RR-src at Inhibitor Concentration ()
<u>42</u>	 (M ₁) 47 (100 μM)	<u>47</u>	 (M ₁) 40 (500 μM)
<u>43</u>	 (M ₁) Ortho: 39 (100 μM) Meta: 89 (100 μM) IC ₅₀ =18 μM, K _i =10 μM Para: 23 (100 μM) NON-ATP COMPETITIVE	<u>48</u>	 (M ₁) Ortho: 43 (100 μM) Meta: 30 (100 μM) Para: 45 (100 μM)
<u>44</u>	 (M ₁) 45 (100 μM)	<u>49</u>	 (M ₁) Ortho: 24 (100 μM) Meta: 74 (100 μM) Para: 54 (100 μM)
<u>45</u>	 (M ₁) 51 (100 μM) IC ₅₀ =170 μM NON-ATP COMPETITIVE	<u>50</u>	 (M ₁ ?) Huang et al 30 (100 μM) Lit. IC ₅₀ =118 nM
<u>46</u>	 (M ₁) Ortho: 42 (100 μM) Meta: In progress Para: 42 (100 μM)	<u>51</u>	 (M ₁ ?) ST 638 37 (100 μM) Lit. IC ₅₀ =18 μM
		<u>52</u>	 (M ₁ ?) Picotarnol 41 (100 μM) Lit. IC ₅₀ =66 μM for p56 ^{lck}

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Inhibitor 50, and analogs (Huang et al., 1995), were of particular interest because the iminochromene scaffold is closely related to the naphthalene scaffold and its binding mode would be expected to be very similar based upon the model (Figure 6). Partly because of this close analogy, the amides of hydroxyanilines with the naphthalene and indole scaffolds were examined as shown in Table V. Also, the modeling studies with these hydroxyaniline amide derivatives in the Src active site indicated that the hydroxyl group may be able to engage in hydrogen bonding interactions with the Src Phe 424-Ala 422 backbone peptide bonds analogous to peptide substrates (see Figure 5). These modeling studies also indicated that the homologous hydroxybenzylamides should be active and, more importantly, provide a substitution position (i.e. the benzylic carbon) for appending side chains to bind in the P-1 side chain pocket (e.g. to Arg 469, Figure 5).

The data in Table V allow the following conclusions to be drawn: 1) Adding an amide extension onto both the naphthalene and indole scaffolds can increase potency as predicted by the models for these scaffolds bound in the Src active site (ca. 5-fold in the cases of 42 vs. 43-meta & 47 vs 48). 2) Adding a hydroxyl group to the naphthalene scaffold adjacent to the amide increases potency (about 5-fold, 43-meta vs. 44) as predicted by the Src model, and also suggests Asn 468 does hydrogen bond with this OH. 3) Moving the M₁ OH group from the position predicted to be best in the Src model to the adjacent position reduces potency by one order of magnitude (43-meta to 45). 4) The indole scaffold is less responsive than the naphthalene scaffold to regiochemistry of the hydroxyaniline extension (48 vs. 43). 5) The naphthalene and the indole scaffolds accept the one carbon homologation provided by using hydroxybenzylamides (46 vs. 43 & 49 vs. 48). 6) The two M₁ hydroxy regioisomers of the naphthalene scaffold are both non-ATP competitive (see Marsilje 2000). 7) All of the methyl hydroxyaniline and hydroxybenzylamide inhibitors were found to be less active suggesting that the hydroxyl group in the amide extension is functioning as a hydrogen bond donor. In this regard it is worth mentioning that in another Src peptide substrate combinatorial library study, Ser and Thr were identified as two of the most preferred residues at the P+2 position (Alfaro-Lopez et al., 1998), suggesting that there are other binding opportunities for an amide extension OH other than to the Phe 424-Ala 422 peptide bonds suggested by the modeling studies. 8) The most

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potent non-ATP competitive, non-peptide, Src inhibitor previously disclosed in the literature (50) is not nearly as potent as reported when tested under the Cellular Mimetic assay conditions (IC_{50} =118 nM reported by Huang et al., 1995 vs only 30% inhibition at 100 μ M) and is less potent than a number of the current inhibitors

5 (especially 43-meta) including the most analogous inhibitor (50 vs. 45). The structure-activity-relationship (SAR) reported for hydroxy regioisomers of 50 in their assay (Huang et al., 1995) also does not correspond with the SAR which was obtained for the related naphthalene inhibitors. For example, their iminochromene analog of the most potent naphthalene inhibitor 43-meta is 230-fold less potent than 50 in their

10 Src assay. An important advantage of the naphthalene scaffold over the iminochromene scaffold is that it allows a highly desirable S_2 specificity element to be added for accessing the P-1 hydrophobic site (see Figure 6) whereas the analogous position can not be substituted on the iminochromene scaffold because it is occupied by the ring oxygen atom.

15 The inhibitor potencies in the Src Cellular Mimetic assay can be further calibrated against other literature non-ATP, non-peptide Src inhibitors. Two additional examples are 51 (ST 638, Shiraishi et al., 1989) which is a member of the "tyrphostin" family of erbstatin analogs (see Lawrence & Niu, 1998) and the natural product PTK inhibitor piceatannol 52 (Thakkar et al., 1993). In the Cellular Mimetic

20 assay all of these known inhibitors are less potent than had been reported suggesting that the assay is particularly demanding in terms of achieving high potency. The initial testing of Src inhibitors is carried out using a single concentration (in triplicate) because commercial Src is too expensive to do full IC_{50} curves on every inhibitor. It should be mentioned, however, that an IC_{50} dose response curve is not linear and the

25 difference between ca. 50% inhibition at 100 μ M and a ca. 90% inhibition at 100 μ M is actually a factor of 10 and not a factor of 2 (e.g. 45 vs. 43-meta). Consequently, the literature Src inhibitors 50-52 are greater than an order-of-magnitude less active than the currently most potent inhibitor 43-meta.

The discrepancies found within the literature reporting the potency of these

30 inhibitors, the sensitivity to assay conditions described earlier with the PKA inhibitors, and the lack of consistency among numerous labs and commercial protein kinase assay kits highlights this overlooked, but crucial, problem in the field.

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Although the inhibitors produced by the present invention may be more potent under other assay conditions, the Cellular Mimetic assay should be used, which mimics the intracellular physical chemical conditions as closely as possible, as the primary potency and rank order guide for evaluating the inhibitors before choosing
5 compounds to proceed to whole cell or tissue assays. As will be discussed in more detail later, the most potent naphthalene-based inhibitor thus far from the Cellular Mimetic assay (i.e. 43-meta, $IC_{50}=18\ \mu M$ and $K_i = 10\ \mu M$) is also effective in specifically blocking pp60^{v-src} stimulated cell proliferation with a similar IC_{50} of ca. 25 μM . This suggests that not only is the Cellular Mimetic Src assay predictive, but
10 also that this class of naphthalene-based inhibitors can readily pass through cell membranes and inhibit intracellular Src.

Analog of a number of the naphthalene and indole inhibitors above can be prepared with the boronic acid or halogen M_1 group in place of the M_1 OH and/or with a S_2 hydrophobic specificity element attached for binding in the Src P-1 site as
15 illustrated in Figures 6 and 7. The naphthalene and indole scaffolds can then be taken through to Step 3 as described below. Each time Step 2 is repeated with new scaffolds from Step 1, the best selectivity elements S_2 and/or S_3 which have discovered with previous scaffolds will be used in the combinatorial libraries of Step 3. Even though the optimal combination of M_1 , S_2 , and S_3 is likely to be different for
20 each scaffold, those found optimal with the previous related scaffold (e.g. going from the naphthalene to the indole scaffold) should be suitable for utilization as better initial specificity elements in Step 2 with the new scaffold. The same process will be repeated each time there is a need to try another scaffold until sufficient potency, selectivity, and suitable pharmaceutical properties are achieved for the Src inhibitors
25 or, subsequently, for inhibitors of additional therapeutically important PTK's.

Some of the chemistry used to prepare the naphthalene inhibitors is described in Marsilje 2000. For attaching a boronic acid functionality in place of a M_1 hydroxyl group in the Src inhibitors from Table V, the Pd (0)-catalyzed cross-coupling methodology was used wherein either an aryl triflate (Ishiyama et al., 1997) or an aryl
30 halide (Ishiyama, 1995) can be coupled with the commercially available pinacol ester of diboron. An illustrative example recently completed is given in Figure 8.

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The example shown in Figure 8 demonstrates that it is possible to selectively triflate the less hindered OH at the M₁ position and this has been proven by its removal to 56 with subsequent ¹H NMR verification of the substitution pattern. The monotriflate 53 was then taken on to the desired boronic acid 55 as indicated. The
5 same reaction sequence also works well for the regioisomer of 42 which corresponds to inhibitor 45 from Table V. The synthetic scheme shown in Figure 9 can be followed, in order to attach hydrophobic S₂ selectivity elements to the naphthalene scaffold.

The naphthalene chemistry can be converted to the solid phase in preparation
10 for synthesizing combinatorial libraries of this scaffold in a 96-well plate format. Thus far, model chemistry has been carried out on the less active naphthalene regioisomer represented by 44 because this compound is readily obtained from commercially available 3,5-dihydroxy-2-naphthoic acid as described in Marsilje 2000. The successful model reactions to date are shown in Figure 10.

15 These model reactions demonstrate that it is possible to couple the naphthalene scaffold to the Wang resin (63) and then carry out chemistry on the triflate [in this case the Pd(0)-catalyzed cross-coupling to the boronic ester 64] followed by cleavage under mild conditions (65). The ester in 63 can also be saponified for subsequent coupling reactions to form amides containing the S₃
20 selectivity elements.

The naphthalene scaffold currently provides three diversity sites to be explored in the combinatorial libraries, M₁, S₂, and S₃. Solid phase combinatorial chemistry with 96-well plate reactors similar to that used in previous studies may be used (Pavia et al., 1996). The greatest number and diversity of side chains will be
25 used for S₃ followed by S₂ and then M₁ for the reasons discussed earlier. One possible overall synthetic strategy, based upon the synthetic model studies above, for preparing these libraries is shown in Figure 11.

Of course if problems arise with this route there are many other possibilities. For example, if the Mitsunobu coupling to give 67 proceeds in too low a yield (due to
30 the increased steric congestion of the added adjacent allyl group-but perhaps not a problem given the 92% loading obtained in Figure 10), then the scaffold could be tethered to a resin through the carboxyl group, rather than the OH, using the

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acylsulfonamide "safety catch" linker (Backes et al., 1996) and form the amides last (the excess amines can be removed after cleavage by filtering through an acidic resin). Likewise, other linkers and/or resins can be used if the reduction of the alkene in the presence of benzylic ethers (67 to 68) is desired but problematic. The first use of the chemistry proposed in Figure 11 will be to simply prepare a library of 96 amides, containing the boronic acid M₁ group, without having the allyl side chain in place so that these two potential complications will not be a problem initially and the most promising S₃ elements can be quickly identified.

At least 14 S₂ hydrophobic side chains (includes linear, branched and cyclic) are identified for further study (28 if the corresponding alkenes are also explored) based upon the modeling of candidate side chains into the P-1 site of the Src model (Figure 6) and on the commercial availability of the needed halides to prepare the corresponding Wittig reagents. At least 96 commercially available amines are available which will provide potential S₃ specificity elements including: 1) hydrocarbons (4), 2) alkyl groups containing hydrogen bond acceptors (4), 3) alkyl groups containing both hydrogen bond acceptors and donors (19), 4) alkyl/aryl groups containing hydrogen bond acceptors and donors (25), 5) aryl hydrogen bond acceptors and donors (10), 6) heterocyclic hydrogen bond acceptors and donors (20), 7) side chains containing cationic groups (4), 8) side chains containing anionic groups (9), and the 3-amino phenol side chain from inhibitor 43-meta as an internal control for Src activity. A broad range of amines were included for S₃, in order not to overly bias the library here due to the higher level of uncertainty for this binding site in the Src model.

The indole scaffold can be developed into a combinatorial library in much the same fashion. In this case, the indole NH would be used as the tether point for attachment to the Wang (or other) resin since the analogous Mitsunobu reaction is known (Bhagwat & Gude, 1994). A large amount of synthetic methodology has been developed for the synthesis of substituted indoles and have designed a route to include the S₂ hydrophobic side chain (see Figure 7) (Ezquerria et al., 1996).

The triflate functionality formed in reaction 2 from intermediate 69 (Figure 11) can be converted to an amine (Wolfe et al., 1997) and then a series of amides or other amine derivatives following the reaction sequence shown in Figure 12. In fact,

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the triflate is a versatile synthetic handle and could be converted into other functional groups as well.

When the amine 72 is available, the known M_1 's (e.g. the sulfamic acid from Src inhibitor 28 Table V and amide-acid 17 Table III) can be evaluated with this more developed scaffold and evaluate some new amine derivatives as potential M_1 's. For example the hydrated tricarbonyl amide M_1 group shown in structure 73 (and its non-hydrated precursor) is accessible via the synthetic methodology (see Lai et al., 1996) and could form a variety of interesting interactions with the conserved catalytic residues.

Following the modeling procedure described above, a series of hydroxy-containing analogs of the boronic acid M_1 group shown in Figure 13 were modeled in the Src and IRTK active sites and the illustrated interactions/binding modes were found as some of the interesting possibilities. By phosphorylating the boronic acid, additional interesting possibilities are available (e.g. suicide type inhibition via reaction of the resulting mixed anhydride with an active site nucleophile). The presence of additional hydroxyl groups on the Tyr-mimetic phenyl ring is necessary and common among many PTK inhibitors (e.g. Piceatannol 52, Table V) and was shown to be beneficial on the side chain with the PKA phosphonate inhibitors (e.g. 2 vs. 3 and 4, Table I). Consequently, adding one or more OH's to the boronic acid inhibitor M_1 design as illustrated in Figure 13 may considerably enhance potency. These OH groups would also extend the boronic acid side chain past the catalytic Asp and Arg residues without suffering a penalty for covering them with hydrocarbon as was probably the case with the PKA boronic acid homologs (23 and 24, Table III). One possible route to the hydroxyboronic acids 76 and 77 utilizes the chiral boronic ester homologation methodology of Matteson (e.g. see Matteson et al., 1987, 1988 & 1990).

Thus, in a preferred embodiment of the invention, the first module is produced by attaching the first module to a peptide scaffold. One or more functional groups are identified which preferentially bind to catalytic residues of the protein kinase, wherein at least one of the one or more functional groups is a halogen. Further, the first module is combined with the second module so that the second module substitutes for the peptide scaffold.

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Preferred first modules have a two or more functional groups, including a halogen and one or more additional functional groups such as a boronic acid group, a hydroxyl group, phosphonic acid, sulfamic acid, a guanidino group, carboxylic acid, an aldehyde, an amide, and hydroxymethylphosphonic acid. More preferred additional functional groups are boronic acid groups, a hydroxyl group, or an amide group. An even more preferred amide group is a vicinal tricarbonyl amide.

Preferred second modules include indole, naphthalene, biphenyl, isoquinoline, benzofuran, and benzothiophene. More preferred second modules are an indole or naphthalene. In some embodiments of the invention more than one first module may be bound to the second module. In addition, the first module may have a linear chain comprising between one and three carbon atoms which links the first module to the second module. In alternative embodiments, one of the carbon atoms in the linear chain is substituted with a nitrogen, oxygen or sulfur atom.

The methods and compounds of the invention are broadly applicable to any protein kinase. Preferred protein kinases are protein tyrosine kinases and protein serine kinases (a.k.a. serine-threonine kinases). Preferred protein tyrosine kinases are pp60^{c-src}, p56^{lck}, p55^{fyn}, ZAP kinase, platelet derived growth factor receptor tyrosine kinase, Bcr-Abl, VEGF (vascular endothelial growth factor) receptor tyrosine kinase, epidermal growth factor receptor tyrosine kinase, and epidermal growth factor receptor-like tyrosine kinases. A more preferred protein tyrosine kinase is pp60^{c-src}. Preferred serine protein kinases include MAP (mitogen activated protein) kinase, protein kinase C, and CDK (cyclin dependent protein kinase).

The method of the present invention may further consist of adding one or more specificity side chain elements to the combination of the first and second modules, as described above. Specificity side chains can increase potency and specificity of the inhibitor. Suitable specificity side chains are described above (R groups for above structures) and in the Examples, which follow.

Once a promising second module is identified it is not necessary to repeat all the steps of the method. Rather, the first module, specificity side chains, or a combination the two may be modified to improve the original inhibitor, i.e an inhibitor which has an increased ability to inhibit protein kinase activity when compared to the unmodified first inhibitor.

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The present method is designed to preferentially provide protein kinase inhibitors which do not act by inhibiting ATP binding to the protein kinase. Inhibitors of protein kinases which act by inhibiting ATP binding may be potent but often lack specificity and are therefore often not good drug candidates. Therefore, protein kinase inhibitors which inhibit protein kinase activity but do not inhibit or only weakly inhibit ATP binding to the protein kinase are preferred.

In another embodiment, the present invention provides a method of inhibiting a protein kinase. The protein kinase is contacted with a compound having at least one first module which has one or more functional groups capable of covalently or non-covalently binding to catalytic residues of the protein kinase, wherein the functional groups comprise a halogen, and a second module which provides a non-peptide scaffold. The combination of the at least one first module and second module inhibits the protein kinase activity.

The present invention further provides a method of treating a condition, responsive to a protein kinase inhibitor, in a subject. An effective dose of a protein kinase inhibitor is administered to a subject. The protein kinase inhibitor has at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein kinase, wherein one or more functional groups comprise a halogen, and a second module which provides a non-peptide scaffold, where the combination of the at least one first module and second module inhibits protein kinase activity.

Another aspect of the present invention is a method for identifying inhibitors of protein phosphatases. The method involves providing at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein phosphatase, combining at least one first module with at least one second module which provides a non-peptide scaffold to form one or more combinations of the first and second modules, screening the one or more combinations of the first and second modules for protein phosphatase inhibition, and selecting combinations of the first and second modules which inhibit protein phosphatase activity.

Suitable first and second modules and functional groups are described above. In a preferred embodiment, the at least one first module comprises a halogen, most

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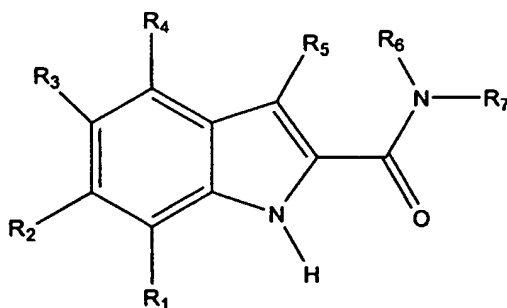
preferably, fluorine. Examples of suitable non-peptide protein phosphatase inhibitors are shown in Table VIII, below.

Suitable protein phosphatases include, but are not limited to, PTP-1B. Other suitable protein phosphatases are described, for example, in Zhang, 2002; McCluskey et al., 2002a; Zhang 2001; McCluskey et al., 2001; Pestell et al., 2000; Moller et al., 2000; Ripka, 2000; Kennedy, 1999; Johnson et al., 2002; McCluskey 2002b.

As described above, this method is designed to preferentially provide phosphatase inhibitors which bind to the substrate peptide binding site.

The present invention also relates to a method of inhibiting a protein phosphatase. The protein phosphatase is contacted by a compound comprising at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein phosphatase, and a second module which provides a non-peptide scaffold. The combination of at least one first module and second module inhibits the protein phosphatase activity.

In one embodiment, the compound has the following formula:



wherein R_1 through R_7 may be the same or different, and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic, or unbranched), preferably having from one to 20 carbon atoms, optionally containing a double or triple bond and optionally substituted with a heteroatom or other functional groups,

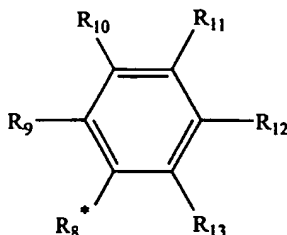
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such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl, or R_5 and R_6 together form a heterocyclic compound. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic, or unbranched), optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that any of R_1 through R_7 and R_a through R_c may be substituted or unsubstituted. In a preferred embodiment, R_3 is a halogen, most preferably, fluorine.

In another embodiment, at least one of R_6 or R_7 is



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wherein R_8^* is the point of attachment and is $(CH_2)_x$, wherein X is from 0 to 10, CH_2CHOH , $CH(CH_3)R$, or $CH(CH_3)S$, and each of R_9 through R_{13} may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic, or unbranched), preferably having from one to 20 carbon atoms, optionally containing a double or triple bond and optionally substituted with a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone,

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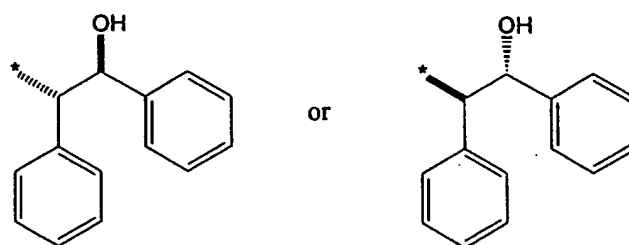
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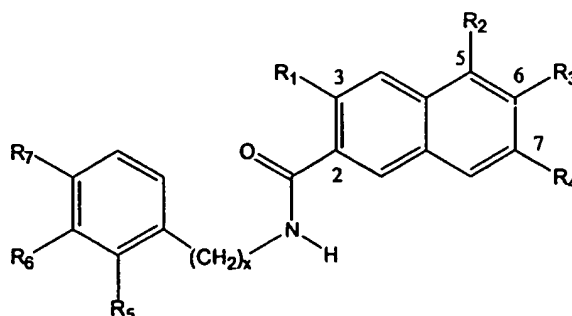
- phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic, or unbranched), optionally substituted with a heteroatom
- 5 or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that any of R_9 through R_{13} and R_a through R_c may be substituted or unsubstituted. In a preferred embodiment, each of R_9 through
- 10 R_{13} may be selected from the group consisting of OCH_3 , OCH_2CH_3 , H, CH_3 , OH , CH_2OH , CF_3 , OCF_3 , CFO , C_6H_5 , OC_6H_5 , $OCH_2C_6H_5$, $OCH_2CH_2CH_3$, CHO , CO_2H , CO_2CH_3 , CH_2CO_2H , $CH_2CO_2CH_3$, NO_2 , and halogen.

In a further embodiment, at least one of R_6 or R_7 is



- 15 wherein the asterisk indicates the point of attachment to the nitrogen.

In yet a further embodiment, the compound has the formula:



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wherein R_1 through R_7 are each the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
5 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic, or unbranched), preferably having from 1 to 20 carbon atoms, optionally containing a double or triple bond and optionally substituted with a heteroatom or other functional groups, such as
10 a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic, or unbranched),
15 optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain
20 further substitutions.

Another aspect of the present invention relates to a method of treating a condition, responsive to a protein phosphatase inhibitor, in a subject. A protein phosphatase inhibitor is administered to a subject. The protein phosphatase inhibitor has at least one first module having one or more functional groups each capable of
25 covalently or non-covalently binding to catalytic residues of the protein phosphatase, and a second module which provides a non-peptide scaffold. The combination of at least one first module and second module inhibits protein phosphatase activity in the subject.

Protein phosphatase inhibitors may be used in various therapeutic techniques,
30 including, but not limited to, treatment of Type II diabetes, obesity, and cancer (Zhang, 2002; McCluskey et al., 2002a; Zhang 2001; McCluskey et al., 2001; Pestell

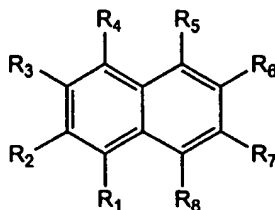
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et al., 2000; Moller et al., 2000; Ripka, 2000; Kennedy, 1999; Johnson et al., 2002; McCluskey 2002b).

Examples of other suitable compounds for the above-described and following methods of the invention include:



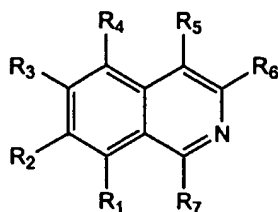
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wherein any of the individual R's can be a halogen-containing M₁, and the remaining R groups can be H, C(O)R_a, C(O)NR_aR_b, C(O)OR_a, C(O)SR_a, OH, OR_a,
 10 OC(O)R_a, OC(O)OR_a, NH₂, NR_aR_b, NR_aC(O)R_b, NR_aC(O)NR_bR_c, NR_aC(O)OR_b,
 NR_aC(O)SR_b, NR_aS(O)R_b, NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b,
 NR_aP(O)OR_bOR_c, NR_aP(O)OR_bR_c, NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a,
 S(O)OR_a, S(O)₂OR_a, S(O)NR_aR_b, S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl,
 heteroaryl, biaryl, and alkyl group (branched, cyclic or unbranched) optionally
 15 containing a double or triple bond and/or a heteroatom or other functional groups,
 such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide,
 urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic
 acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a, R_b,
 and R_c can be the same or different and are selected from the group consisting of H,
 20 aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic or unbranched)
 optionally substituted with a heteroatom or other functional groups such as a
 carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea,
 urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid,
 phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is
 25 understood that all open substitution positions in the above side chains can contain
 further substitutions;

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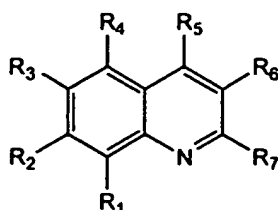
wherein any of the individual R's can be M₁, and the remaining R groups can

5 be H, C(O)R_a, C(O)NR_aR_b, C(O)OR_a, C(O)SR_a, OH, OR_a, OC(O)R_a, OC(O)OR_a, NH₂, NR_aR_b, NR_aC(O)R_b, NR_aC(O)NR_bR_c, NR_aC(O)OR_b, NR_aC(O)SR_b, NR_aS(O)R_b, NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b, NR_aP(O)OR_bOR_c, NR_aP(O)OR_bR_c, NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a, S(O)OR_a, S(O)₂OR_a, S(O)NR_aR_b, S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl, heteroaryl, biaryl, and alkyl group

10 (branched, cyclic or unbranched) optionally containing a double or triple bond and/or a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a, R_b, and R_c can be the same or different

15 and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic or unbranched) optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl,

20 biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions;



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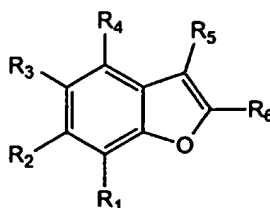
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wherein any of the individual R's can be M_1 , and the remaining R groups can be H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and alkyl group (branched, cyclic or unbranched) optionally containing a double or triple bond and/or a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic or unbranched) optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions;

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wherein any of the individual R's can be M_1 , and the remaining R groups can be H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and alkyl group

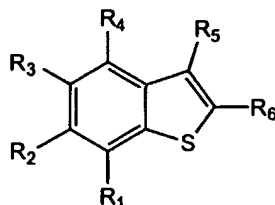
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(branched, cyclic or unbranched) optionally containing a double or triple bond and/or a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic or unbranched) optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions;



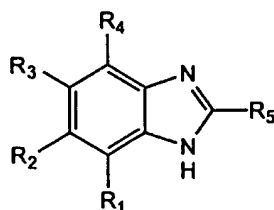
wherein any of the individual R's can be M_1 , and the remaining R groups can be H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and alkyl group (branched, cyclic or unbranched) optionally containing a double or triple bond and/or a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl,

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and alkyl (branched, cyclic or unbranched) optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions;



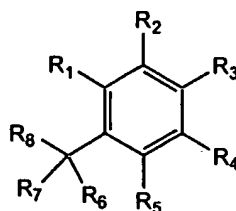
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wherein any of the individual R's can be M₁, and the remaining R groups can be H, C(O)R_a, C(O)NR_aR_b, C(O)OR_a, C(OSR_a), OH, OR_a, OC(O)R_a, OC(O)OR_a, NH₂, NR_aR_b, NR_aC(O)R_b, NR_aC(O)NR_bR_c, NR_aC(O)OR_b, NR_aC(OSR_b), NR_aS(O)R_b, NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b, NR_aP(O)OR_bOR_c, NR_aP(O)OR_bR_c, NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a, S(O)OR_a, S(O)₂OR_a, S(O)NR_aR_b, S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl, heteroaryl, biaryl, and alkyl group (branched, cyclic or unbranched) optionally containing a double or triple bond and/or a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a, R_b, and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic or unbranched) optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions;

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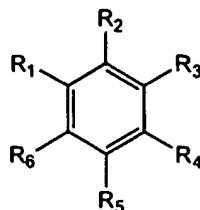
- wherein any of the individual R's can be M_1 , and the remaining R groups can be H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and alkyl group (branched, cyclic or unbranched) optionally containing a double or triple bond and/or a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone,
- 15 phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic or unbranched) optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether,
- 20 thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions;

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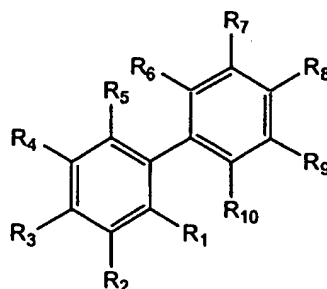


- wherein any of the individual R's can be M₁, and the remaining R groups can be H,
- 5 C(O)R_a, C(O)NR_aR_b, C(O)OR_a, C(O)SR_a, OH, OR_a, OC(O)R_a, OC(O)OR_a, NH₂,
 NR_aR_b, NR_aC(O)R_b, NR_aC(O)NR_bR_c, NR_aC(O)OR_b, NR_aC(O)SR_b, NR_aS(O)R_b,
 NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b, NR_aP(O)OR_bOR_c, NR_aP(O)OR_bR_c,
 NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a, S(O)OR_a, S(O)₂OR_a, S(O)NR_aR_b,
 S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl, heteroaryl, biaryl, and alkyl group
- 10 (branched, cyclic or unbranched) optionally containing a double or triple bond and/or
 a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester,
 alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone,
 phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid,
 aryl, heteroaryl, biaryl, and heterobiaryl. R_a, R_b, and R_c can be the same or different
- 15 and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl,
 and alkyl (branched, cyclic or unbranched) optionally substituted with a heteroatom or
 other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether,
 thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid,
 phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl,
- 20 biaryl, and heterobiaryl. It is understood that all open substitution positions in the
 above side chains can contain further substitutions;

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wherein any of the individual R's can be M₁, and the remaining R groups can be H, C(O)R_a, C(O)NR_aR_b, C(O)OR_a, C(O)SR_a, OH, OR_a, OC(O)R_a, OC(O)OR_a, NH₂, NR_aR_b, NR_aC(O)R_b, NR_aC(O)NR_bR_c, NR_aC(O)OR_b, NR_aC(O)SR_b, NR_aS(O)R_b, NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b, NR_aP(O)OR_bOR_c, NR_aP(O)OR_bR_c, NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a, S(O)OR_a, S(O)₂OR_a, S(O)NR_aR_b, S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl, heteroaryl, biaryl, and alkyl group (branched, cyclic or unbranched) optionally containing a double or triple bond and/or a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a, R_b, and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic or unbranched) optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that all open substitution positions in the above side chains can contain further substitutions.

The present invention also provides a method for testing compounds for an ability to inhibit protein kinase or protein phosphatase activity. Compounds are produced as described above. The activity of the protein kinase or protein phosphatase is measured in the presence of the inhibitor at the same temperature, pH, ionic strength, osmolarity, and free magnesium concentration as found in a cell which expresses the protein kinase or protein phosphatase. The level of protein kinase or protein phosphatase activity is compared to the level of activity from the protein

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kinase or protein phosphatase without the presence of the inhibitor. Such an assay system which mimics physiological conditions provides the most relevant inhibition data. The assay may be conducted in an automated assay system. Furthermore, the assay may be combined with a combinatorial chemistry method to rapidly screen
5 numerous candidates.

The Pierce 96-well plate non-radioactive ELISA PTK assay method may be adapted to the Cellular Mimetic assay conditions for initial Src screening of the 96-well plate combinatorial libraries. This high throughput assay utilizes the same RR-SRC peptide substrate, except that it is biotinylated so that it can be attached to the
10 NeutrAvidin-coated wells in their commercial 96-well plates. This high throughput inhibition assay can be run by incubating Src with the RR-SRC substrate prebound to the wells followed by adding their anti-phosphotyrosine antibody (PY20)-horseradish peroxidase (HRP) conjugate and their HRP substrate to quantitate the level of phospho-RR-SRC produced via measuring the level of HRP product with a 96-well
15 plate UV reader. Standard low throughput P^{32} -ATP radioactive assays have been used, but a 96-well plate format is preferred, especially with a non-radioactive assay if possible. As very potent Src inhibitors are developed, a panel of protein kinase assays could be set up with commercially available protein kinases, using the Cellular Mimetic protein kinase assay conditions, and test these inhibitors across the panel to
20 obtain an initial assessment of specificity. A more complete specificity assessment, involving the full ca. 2,000 protein kinases, will need to be conducted in cell culture and *in vivo*.

Active Src inhibitors can be studied in a set of side-by-side cell-based assays using normal rat kidney (NRK) cells and a temperature-sensitive pp60^{v-Src}
25 transformant of this cell line (LA25). The LA25 transformant engages in anchorage- and serum-independent growth at the "permissive" temperature of 33°C due to activation of pp60^{v-Src} but not at the "non-permissive" temperature of 40°C at which pp60^{v-Src} is not activated (Li et al., 1996). The use of this pair of closely related cell lines for testing the Src inhibitors at both the permissive and non-permissive
30 temperatures allows one to determine if a given Src inhibitor is blocking cell growth due to specific blockade of the Src signaling pathway, by a different mechanism or by

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a general cytotoxic effect. Results from initial testing of the non-peptide Src inhibitor 43-meta (Table V) in this pair of cell lines are shown in Figure 14.

As shown in this graph the growth of the LA25 cells at the permissive temperature of 33°C is inhibited by ca. 50% at a 25 µM concentration of 43-meta relative to the LA25 cell growth at the non-permissive 40°C as a control. The lack of cell toxicity of 43-meta is evidenced by the fact that as its concentration is increased up to 400 µM, the basal growth of the NRK non-transformed cells, the LA25 cells at the non-permissive 40°C, and the LA25 cells at the permissive temperature of 33°C (but with pp60^{v-src} fully inhibited by 43-meta) not only does not decrease but actually increases somewhat (presumably due to a non-Src related activity of this compound). Since the 43-meta solutions were prepared with a low concentration of DMSO for solubilization, a DMSO control was also run at the same concentration.

Moreover, promising Src inhibitors can be screened in primary human tumor tissue assays, particularly to look for synergy with other known anti-cancer drugs.

Another aspect of the present invention relates to a method for protecting against or treating hearing loss in a subject. This method involves administering an effective amount of a protein tyrosine kinase (PTK) inhibitor to the subject to protect against or to treat hearing loss.

The PTK inhibitor in the above method of the present invention may be a receptor tyrosine kinase inhibitor or a non-receptor tyrosine kinase inhibitor (see Hubbard et al., 2000). In a preferred embodiment of the present invention, the PTK inhibitor is a Src family PTK inhibitor. In this embodiment, the PTK inhibitor may inhibit the activity of any member of the Src family, including pp60^{c-src} tyrosine kinase. In another preferred embodiment, the PTK inhibitor is a focal adhesion kinase inhibitor.

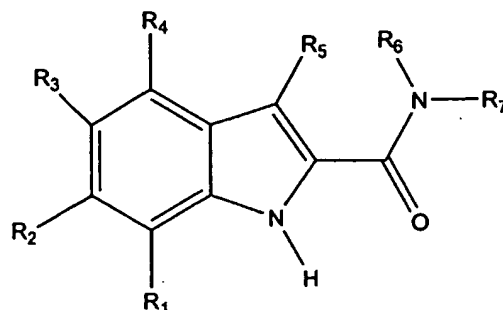
In one embodiment, the PTK inhibitor is a non-peptide PTK inhibitor. In a preferred embodiment, the non-peptide PTK inhibitor has at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein kinase and a second module which provides a non-peptide scaffold. The combination of the first and second modules inhibits protein kinase activity in the subject.

For example, suitable non-peptide PTK inhibitors have the following formula:

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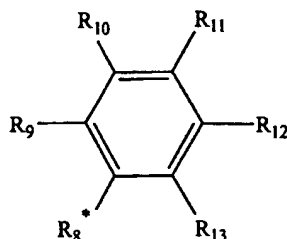
wherein R_1 through R_7 may be the same or different, and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 5 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl,
 10 heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic, or unbranched),
 preferably having from 1 to 20 carbon atoms, optionally containing a double or triple
 bond and optionally substituted with a heteroatom or other functional groups, such as
 a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea,
 urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid,
 phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl, or R_5 and R_6
 15 together form a heterocyclic compound. R_a , R_b , and R_c can be the same or different
 and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl,
 and alkyl (branched, cyclic, or unbranched), optionally substituted with a heteroatom
 or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether,
 thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid,
 20 phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl,
 biaryl, and heterobiaryl. It is understood that all open substitution positions in the
 above side chains can contain further substitutions. Examples of suitable R_6 and R_7
 groups are provided in Table VI, below. In a preferred embodiment, R_3 is a halogen,
 most preferably, fluorine.

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In one embodiment, at least one of R_6 or R_7 is



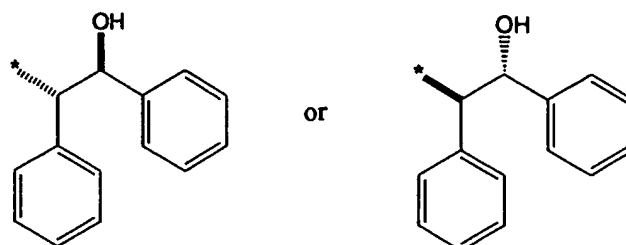
- wherein R_8^* is the point of attachment and is $(CH_2)_x$, wherein X is from 0 to 10, CH_2CHOH , $CH(CH_3)R$, or $CH(CH_3)S$, and each of R_9 through R_{13} may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(OSR_a)$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic, or unbranched), preferably having from 1 to 20 carbon atoms, optionally containing a double or triple bond and optionally substituted with a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic, or unbranched), optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is understood that any of R_9 through R_{13} and R_a through R_c may be substituted or unsubstituted. In a preferred embodiment, each of R_9 through R_{13} may be selected from the group consisting of OCH_3 , OCH_2CH_3 , H, CH_3 , OH, CH_2OH , CF_3 , OCF_3 , CFO , C_6H_5 , OC_6H_5 , $OCH_2C_6H_5$, $OCH_2CH_2CH_3$, CHO , CO_2H , CO_2CH_3 , CH_2CO_2H , $CH_2CO_2CH_3$, NO_2 , and halogen.

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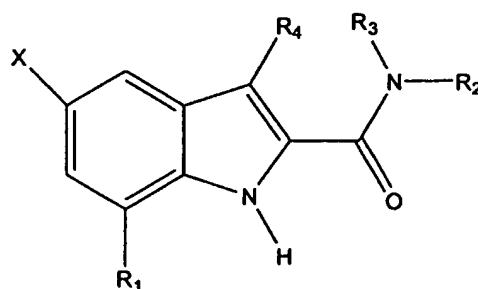
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In another embodiment, at least one of R_6 or R_7 is



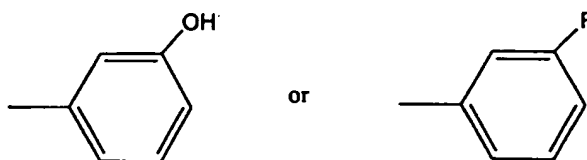
wherein the asterisk indicates the point of attachment to the nitrogen.

- 5 Another non-peptide PTK inhibitor useful in the method of the present invention has the following formula:



- 10 wherein X is a halogen, preferably, fluorine, and R_1 through R_4 are specificity elements.

In one embodiment, R_1 is H, R_2 is



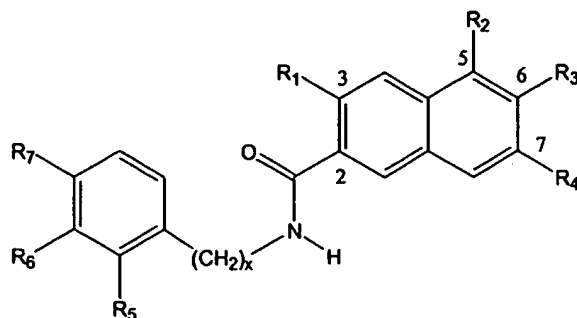
- 15 R_3 is H, and R_4 is H. The compound may also be substituted at any other position on the indole ring.

A further non-peptide PTK inhibitor has the formula

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wherein R_1 through R_7 are each the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 5 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and alkyl (branched, cyclic, or unbranched), preferably having from 1 to 20 carbon atoms, optionally containing a double or triple
 10 bond and optionally substituted with a heteroatom or other functional groups, such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. R_a , R_b , and R_c can be the same or different and are selected from the group consisting of H, aryl,
 15 heteroaryl, biaryl, heterobiaryl, and alkyl (branched, cyclic, or unbranched), optionally substituted with a heteroatom or other functional groups such as a carboxylic acid, carboxylic ester, alcohol, ether, thioether, amide, thioamide, urea, urethane, sulfoxide, sulfone, phosphonic acid, phosphonic ester, phosphinic acid, phosphinic ester, boronic acid, aryl, heteroaryl, biaryl, and heterobiaryl. It is
 20 understood that all open substitution positions in the above side chains can contain further substitutions. X is preferably 0 or 1.

In yet another embodiment, the PTK inhibitor is a peptide protein tyrosine kinase inhibitor. Suitable peptide PTK inhibitors are described, for example, in Lai et al., 1998.

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In one embodiment, the PTK inhibitor in this method of the present invention is a peptide substrate directed inhibitor. As used herein, a peptide substrate directed inhibitor is an inhibitor which binds to the peptide substrate specificity sites of the active site of the tyrosine kinase and does not bind to ATP. The above-described non-
5 peptide PTK inhibitors are examples of peptide substrate directed inhibitors.

In another embodiment, the PTK inhibitor is an ATP site directed inhibitor. As used herein, an ATP site directed inhibitor is an inhibitor that binds ATP to competitively inhibit a PTK. Examples of ATP site inhibitors include, but are not limited to, flavanoids, genistein, and lavendustin A. Examples of ATP site inhibitors
10 (antagonists) are disclosed, for example, in Levitzki and Gazit, 1995.

In yet another embodiment, the PTK inhibitor is Src homology 2 (SH2) site inhibitor. An SH2 site inhibitor binds to the SH2 site to inhibit the activity of the PTK. Examples of suitable SH2 inhibitors are described, for example, in Garcia-Echeverria, 2001, Muller, 2001, Fretz et al., 2000, and Vu, 2000.

15 In a further embodiment, the PTK inhibitor is a Src homology 3 (SH3) site inhibitor. An SH3 site inhibitor binds to the SH3 site to inhibit the activity of the PTK. Examples of suitable SH3 inhibitors are described, for example, in Stein, 1998 and Sparks et al., 1994.

In another embodiment, the PTK inhibitor is an allosteric inhibitor. As used
20 herein, an allosteric inhibitor binds to an allosteric site other than the active site of the PTK, thereby changing the conformation of the PTK and inhibiting activity of the PTK.

The above PTK inhibitors may bind covalently or non-covalently (and reversibly or irreversibly) to their respective sites.

25 The PTK inhibitors can be administered orally (e.g., in food), parenterally, subcutaneously, intravenously, intramuscularly, intraperitoneally, by intranasal instillation, by intracavitary or intravesical instillation, intraauditorily, intraarterially, intralesionally, by metering pump, or by application to mucous membranes. They may be administered alone or with pharmaceutically or physiologically acceptable
30 carriers, excipients, or stabilizers, and can be in solid or liquid form, such as tablets, capsules, powders, solutions, suspensions, or emulsions.

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The solid unit dosage forms can be of the conventional type. The solid form can be a capsule, such as an ordinary gelatin type containing the PTK inhibitor and a carrier, for example, lubricants and inert fillers, such as lactose, sucrose, or cornstarch. In another embodiment, these PTK inhibitors can be tableted with
5 conventional tablet bases, such as lactose, sucrose, or cornstarch, in combination with binders, like acacia, cornstarch, or gelatin, disintegrating agents, such as cornstarch, potato starch, or alginic acid, and lubricants, like stearic acid or magnesium stearate.

The PTK inhibitors may also be administered in injectable dosages by solution or suspension of these materials in a physiologically acceptable diluent with a
10 pharmaceutical carrier. Such carriers include sterile liquids, such as water and oils, with or without the addition of a surfactants, adjuvants, excipients, or stabilizers. Illustrative oils are those of petroleum, animal, vegetable, or synthetic origin, for example, peanut oil, soybean oil, or mineral oil. In general, water, saline, aqueous dextrose and related sugar solutions, and glycols, such as propylene glycol or
15 polyethylene glycol, are preferred liquid carriers, particularly for injectable solutions.

For use as aerosols, the PTK inhibitor in solution or suspension may be packaged in a pressurized aerosol container together with suitable propellants, for example, hydrocarbon propellants like propane, butane, or isobutane, and with conventional adjuvants. The PTK inhibitor can also be administered in a non-
20 pressurized form, such as in a nebulizer or atomizer.

Suitable dosages are determined based on a variety of factors, but may include from about 50 mg/kg to about 1000 mg/kg of PTK inhibitor, preferably from about 50 mg/kg to about 400 mg/kg of PTK inhibitor (see, e.g., Bakhtiar et al., 2002; Druker, 2002).

25 The PTK inhibitors described herein may be administered to any subject, such as any member of the class Mammalia including, without limitation, humans and non-human primates, such as chimpanzees and other apes and monkey species; farm animals including cattle, sheep, pigs, goats and horses; domestic animals including cats and dogs; laboratory animals including rodents, such as mice, rats, and guinea
30 pigs, and the like. The term does not denote a particular age or sex.

As described herein, the PTK inhibitors may be used to protect against or prevent hearing loss in a subject. In order to protect against hearing loss, the PTK

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inhibitor may be administered prior to noise exposure or exposure to a drug which induces hearing loss. Such drugs may include chemotherapeutic drugs (e.g., platinum-based drugs which target hair cells) and aminoglycoside antibiotics.

Alternatively, the PTK inhibitors may be used to treat hearing loss in a subject. In this embodiment, the PTK inhibitor is administered to the subject subsequent to the initiation of hearing loss to reduce the level of hearing loss.

Although not wishing to be bound by theory, it is believed that the administration of PTK inhibitors prevents apoptosis of cochlear hair cells, thereby preventing hearing loss. In particular, following noise exposure, the tight cell junctures between the cochlear hair cells, as well as the cell-extracellular matrix interaction, are torn and stressed. The stressing of these tight cell junctures initiates apoptosis in the cells through a complex signaling pathway, in which the Src family of PTKs act as molecular switches, interacting with focal adhesion kinase to transduce signals of cell-matrix disruptions to the nucleus. It is believed that the administration of PTK inhibitors prevents the initiation of apoptosis in this cascade.

As described above, the inhibitors described herein are inhibitors of pp60c-src, of highly metastatic prostate cancer cell growth, and are non-toxic in mice upon high dose acute i.p. administration. Some of these compounds may be found to have other biological activities upon broader testing (e.g., inhibit glycogen phosphorylase for Type II diabetes, HIV reverse transcriptase, or thromboxane synthase). Thus, these compounds may be used as tyrosine kinase inhibitors in combination therapeutic applications. For example, the PTK inhibitor may be administered to a subject in an amount and under conditions effective to treat or prevent hearing loss and to treat cancer (e.g., where a synergistic activity is found). Tyrosine kinase inhibitors have other potential therapeutic applications as well (e.g., immunosuppressants in the case of p56lck) and inhibitors of the tyrosine phosphatase PTP-1B may provide drugs for treating Type II diabetes. Therefore, the PTK inhibitors disclosed herein may be used in a variety of combination therapies.

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EXAMPLES

Example 1 - Synthesis and Activity of Indole Derivative Protein Kinase and/or Protein Phosphatase Inhibitors

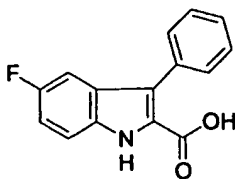
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The following results show the solution phase synthesis of 5-fluoroindole-2-carboxamide libraries and testing of indole derived protein kinase and/or protein phosphatase inhibitors. These final products are examples of indole-based inhibitors wherein synthesis with a 5-fluoro group is illustrated.

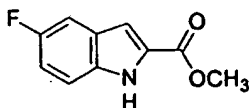
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A. Synthesis of Intermediates and Sample Reagents:

5-fluoro-3-phenylindole-2-carboxylic acid



15 (a) Preparation of Methyl Ester



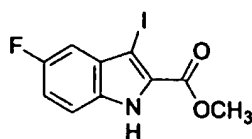
A mixture of 5-fluoroindole-2-carboxylic acid (6 g, 33.5 mmol) and a freshly prepared methanolic HCl (100 mL) was stirred overnight at room temperature. The precipitated ester was collected by filtration, washed with NaHCO₃ saturated solution, water, and MeOH. The filtrate was treated with saturated NaHCO₃ and extracted with EtOAc. The organic layer was washed with brine, dried (MgSO₄), and evaporated *in vacuo*. The product ester (6 g) was an off white solid and it was used for the next step without further purification: MP 200-201 °C; ¹H NMR (CDCl₃, 500 MHz) δ 8.94 (br, 1H), 7.33 (dd, 1H, *J* = 9.2 and 4.3 Hz), 7.30 (dd, 1H, *J* = 2.2 and 9.2), 7.15 (d, 1H, *J* = 2.1 Hz), 7.07 (ddd, 1H, *J* = 2.5, 8.9 and 9.1 Hz), 3.92 (s, 3H)

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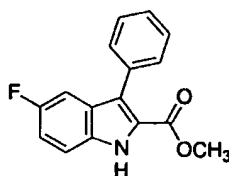
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(b) Preparation of the 3-iodo Derivative

4.22 g (21.8 mmol) of the methyl ester was dissolved in DMF (25 mL). In another flask, a solution of iodine (6.09 g, 24 mmol) and KOH (4.65 g, 82.9 mmol) in DMF (25 mL) was stirred for 30 minutes and added dropwise to the ester solution over 5 minutes. After stirring for 10 minutes at room temperature, the reaction was quenched by pouring into a solution of NaHSO₃ (2.2 g), NH₄OH (25% solution in H₂O) in 300 mL water. The mixture was stirred for 30 minutes then the precipitated solid product was collected by filtration and washed with H₂O: ¹H NMR (CDCl₃, 500 MHz) δ 9.17 (br, 1H), 7.33 (dd, 1H, *J* = 9.0 and 4.2 Hz) 7.21 (dd, 1H *J* = 9.0 and 2.0 Hz), 7.12 (dt, 1H, *J* = 9.0 and 2.0 Hz), 3.81 (s, 3H).

(c) Suzuki Coupling

The iodo derivative was mixed with benzenboronic acid (2.76 g, 22 mmol), PdCl₂(PPh₃)₂ (0.7 g, 1 mmol), and 50 mL of 2M Na₂CO₃ in dioxane (200 mL). The mixture was stirred at 90 °C overnight. The solvent was evaporated under vacuum. The product was extracted with EtOAc (3x200 mL). The combined extract was washed with brine, dried with MgSO₄, and purified by crystallization (CH₂Cl₂-hexane) and silica gel chromatography (Hexane-EtOAc 4:1): MP 189 °C; ¹H NMR (CDCl₃, 500 MHz) δ 8.94 (br, 1H), 7.51 (dd, 2H, *J* = 1.5 and 7.9 Hz), 7.45 (ddd, 2H, *J* = 1.8, 7.3 and 7.8), 7.39-7.34 (complex, 2H), 7.25 (dd, 1H, *J* = 2.5 and 8.7 Hz), 7.10 (ddd, 1H, *J* = 2.5, 8.9 and 9.1 Hz), 3.80 (s, 3H).

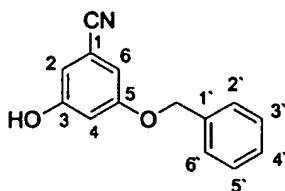
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(d) Saponification Of Methyl Ester

The ester described above (2.5 g, 9.28 mmol) was dissolved in THF (30 mL). A solution of LiOH (2.4 g, 100 mmol) in water (20 mL) was added and the mixture was heated at reflux for 1 hour. The mixture was cooled to room temperature and THF was removed by vacuum evaporation. The mixture was treated with 2M HCl until it became acidic. The product was extracted with EtOAc. The organic layer was washed, dried (brine, Na₂SO₄), and concentrated under vacuum. The crude solid product was redissolved in NaHCO₃ (saturated solution) and washed several times with CH₂Cl₂. The aqueous layer was acidified with ice and 2M HCl and extracted with EtOAc. After washing, drying, and rotavaping, the product was collected as white solid (yield 2.3 g, 97%): MP 195-196 °C; ¹H NMR (CDCl₃, 500 MHz) δ 8.94 (br, 1H), 7.52 (dd, 2H, *J* = 1.8 and 7.9 Hz), 7.46 (ddd, 2H, *J* = 1.8, 7.3 and 7.6), 7.40 (ddd, 1H, *J* = 1.8, 7.4 and 7.8 Hz), 7.37 (dd, 1H, *J* = 9.0 and 4.2 Hz), 7.25 (dd, 1H, *J* = 2.5 and 8.7 Hz), 7.12 (ddd, 1H, *J* = 2.4, 8.8 and 8.9 Hz).

3-benzyloxy-5-hydroxybenzonitrile

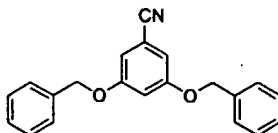
To a mixture of 3,5-dihydroxybenzonitrile (1.08 g, 8 mmol) and K₂CO₃ (1.104 g, 8 mmol) in CH₃CN (50 mL), benzyl bromide (1.438 g, 8 mmol) was added. The mixture was heated to reflux for 2 hours. Solvent was evaporated under vacuum. The residue was treated with EtOAc (200 mL) and 1M HCl (200 mL). The organic layer was washed, dried, and evaporated *in vacuo*. The residue was chromatographed (gradient, Hexanes-CH₂Cl₂-MeOH) to give 3-benzyloxy-5-hydroxybenzonitrile (529 mg, 29%), 3,5-dibenzyloxybenzonitrile (784 mg, 31%) and 256 mg (23.7 mg, 24%) of the starting material. The product 3-benzyloxy-5-hydroxybenzonitrile had: MP 144-145 °C; ¹H NMR δ 9.15 (s, 1H, OH), 7.47 (d, 2H, *J* = 7.0 Hz, 2' and 6'), 7.40 (ddd,

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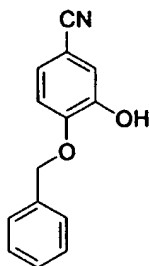
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2H, $J = 7.0, 7.0, 2.0$ Hz, 3' and 5'), 7.34 (dd, 1H, $J = 7.7$ and 2.1 Hz, 4'), 6.89 (dd, 1H, $J = 1.5$ Hz, 4), 6.78 (d, 2H, $J = 1.8$ Hz), 5.16 (s, 2H).

3,5-dibenzoyloxybenzonitrile

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This compound had MP 106 °C; ^1H NMR (CDCl_3 , 500 MHz) δ 7.38 (complex, 10H), 6.83 (d, 2H, $J = 2.1$ Hz), 6.79 (d, 1H, $J = 2.1$ Hz).

10 4-benzoyloxy-3-hydroxybenzonitrile

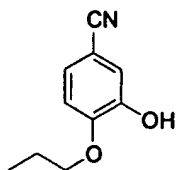
A mixture of 3,4-dihydroxybenzonitrile (540 mg, 4 mmol), K_2CO_3 (552 mg, 4 mmol) and benzyl bromide (476 mg, 4 mmol) in acetone (20 mL) was stirred at room temperature for 3 days. The mixture was evaporated under vacuum and subjected to
15 flash column chromatography (2% MeOH in toluene-hexane, 2:1) to give the desired product (224 mg, 25%): MP 101 °C; ^1H NMR (Acetone- d_6 , 500 MHz) δ 8.55 (s, 1H), 7.50 (d, 2H, $J = 7.3$ Hz), 7.39 (dd, 2H, $J = 7.0$ and 7.3), 7.34 (dd, 1H, $J = 7.0$ and 7.3), 7.2 (m, complex, 3H), 5.25 (s, 2H).

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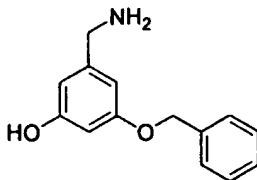
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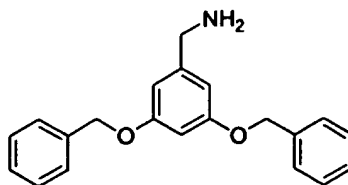
3-hydroxy-4-propyloxybenzonitrile

This compound was prepared following a similar procedure used to prepare 4-benzyloxy-3-hydroxybenzonitrile in 27% yield: MP 99 °C; ¹H NMR (Acetone-*d*₆, 500
5 MHz) δ 8.33 (s, 1H), 7.21 (dd, 1H, *J* = 8.2 and 1.8 Hz), 7.13 (d, 1H, *J* = 1.8 Hz), 7.08 (d, 1H, *J* = 8.3 Hz), 4.07 (t, 2H, *J* = 6.4 Hz), 1.80 (m, 2H), 1.01 (t, 3H, *J* = 7.3 Hz).

3-benzyloxy-5-hydroxybenzylamine

10 3-benzyloxy-5-hydroxybenzonitrile (225 mg, 1 mmol) was dissolved in 2 mL THF. 2 mL of BH₃-THF (1.5 M in THF and ether) was added dropwise, then the mixture was heated at reflux temperature for 3 hours. After cooling, the mixture was carefully poured to 3M HCl (ice cooled) and allowed to stir for 20 hours at room temperature. The mixture was neutralized with solid NaHCO₃, thus the product
15 precipitated as a white solid. The product was collected by filtration, washed with water, and dried (140 mg, 61%): MP 164-166 °C (dec); ¹H NMR (DMSO-*d*₆, 400 MHz) δ 9.28 (br, 1H), 7.41 (d, 2H, *J* = 6.9 Hz), 7.36 (dd, 2H, *J* = 7.0 and 7.6 Hz), 7.30 (dd, 1H, *J* = 7.0 and 6.6 Hz), 6.43 (s, 1H), 6.32 (s, 1H), 6.21 (dd, 1H, *J* = 2.2 and 2.0 Hz), 4.99 (s, 2H), 3.57 (s, 2H).

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3,5-dibenzyloxybenzylamine

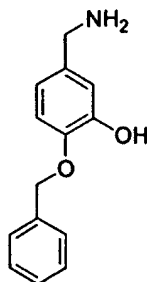
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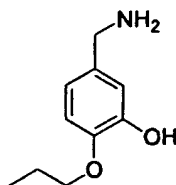
This compound was prepared according to the procedure used in preparation of 3-benzyloxy-5-hydroxybenzylamine. The reaction was quenched via addition of MeOH and the mixture was left to stir overnight. The solvent was removed and the product was obtained by flash column chromatography (CH₂Cl₂–Hexanes containing 5% MeOH) as clear thick oil (90%): ¹H NMR (Acetone-*d*₆, 500 MHz) δ 7.46 (d, 4H, *J* = 7.6), 7.37 (dd, 4H, *J* = 7.3 and 7.6), 7.31 (dd, 2H, *J* = 7.3 and 7.0), 6.65 (d, 1H, *J* = 2.1 Hz), 6.64 (d, 1H, *J* = 2.0 Hz), 6.52 (dd, 1H, *J* = 2.0 and 2.2 Hz), 5.07 (s, 4H), 4.35 (s, 2H), 1.97 (br, 1H), 1.85 (br, 1H).

10 **4-benzyloxy-3-hydroxybenzylamine**



This compound was prepared according to procedure used in preparation of 3,5-dibenzyloxybenzylamine, starting from 4-benzyloxy-3-hydroxybenzonitrile. Yield was 33%. MP 122-125 °C; ¹H NMR (DMSO-*d*₆, 400 MHz) δ 8.9 (br, 1H), 7.44 (d, 2H, *J* = 7.4 Hz), 7.35 (dd, 2H, *J* = 7.0 and 7.7 Hz), 7.28 (dd, 1H, *J* = 7.0 and 7.3), 6.85 (d, 1H, *J* = 7.6 Hz), 6.77 (d, 1H, *J* = 2.1 Hz), 6.61 (dd, 1H, *J* = 7.4 and 2.2 Hz), 5.05 (s, 2H), 3.55 (s, 1H), 2.50 (br, 2H).

3-hydroxy-4-propyloxybenzylamine



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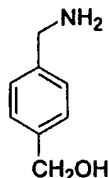
This compound was prepared by reduction of 3-hydroxy-4-propyloxybenzonitrile according to procedure described in preparation of 3,5-dibenzyloxybenzylamine. Yield was 48%; MP 110-113 °C (dec.); ¹H NMR (CDCl₃,

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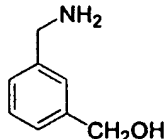
400 MHz) δ 6.86 (s, 1H), 6.77 (d, 1H, $J = 8.4$ Hz), 6.74 (d, 1H, $J = 8.1$ Hz), 3.95 (t, 1H, $J = 6.6$ Hz), 3.74 (s, 2H), 2.01 (br, 2H), 1.82 (m, 2H), 1.02 (t, 3H, $J = 7.4$ Hz).

4-hydroxymethylbenzylamine

5

This compound was prepared by reduction of 4-cyanobenzaldehyde according to the procedure described in preparation of 3,5-dibenzoyloxybenzylamine. Yield was 46%; MP 102-123 °C; ^1H NMR (Acetone- d_6 , 500 MHz) 7.27 (m, complex 4H), 4.58 (s, 2H), 3.72 (s, 2H), 3.69 (s, 1H) 2.77 (br, 1H), 2.45 (br, 1H).

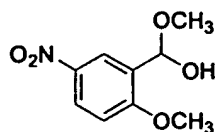
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3-hydroxymethylbenzylamine

15

This compound was prepared by reduction of 3-cyanobenzaldehyde according to the procedure described in preparation of 3,5-dibenzoyloxybenzylamine. Yield was 66%; ^1H NMR (Acetone- d_6 , 500 MHz) δ 7.32 (s, 1H), 7.23 (dd, 1H, $J = 7.6$ and 7.0), 7.19, complex, 2H), 4.59 (s, 2H), 4.40 (s, 2H), 4.10 (br, 1H), 1.96 (br, 1H), 1.88 (br, 1H).

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2-methoxy-5-nitrobenzaldehyde methyl hemiacetal

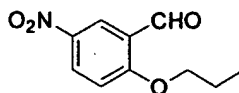
2-hydroxy-5-nitrobenzaldehyde (3.34 g, 20 mmol) was dissolved in acetone (70 mL); K_2CO_3 (5.53 g, 40 mmol) and iodomethane (14.19 g, 100 mmol) was added and the solution heated to reflux overnight. Solvent was removed *in vacuo* and residue was dissolved in EtOAc. The resulting product was washed with 2M NaOH,

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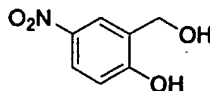
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water, and brine and dried. Removal of solvent resulted in a solid product (2.5 g, 69%) of 2-methoxy-5-nitrobenzaldehyde methyl hemiacetal: MP 147-148 °C (89 °C reported for the aldehyde); ¹H NMR (CDCl₃, 400 MHz) δ 8.43 (d, 1H, *J* = 2.9 Hz), 8.24 (dd, 1H, *J* = 2.6 and 9.1 Hz), 7.78 (d, 1H, 16.5 Hz), 6.99 (d, 1H, *J* = 9.1 Hz), 6.83 (d, 1H, *J* = 16.4 Hz). NOTE: This NMR was taken after about 10 months and the hemiacetal was still existing and pure.

5-nitro-2-propyloxybenzaldehyde

This compound was prepared by the reaction of 2-hydroxy-5-nitrobenzaldehyde and 1-iodopropane using a similar procedure as described in the preparation of 2-methoxy-5-nitrobenzaldehyde methyl hemiacetal. Yield was 72%: MP (51-52 °C); ¹H NMR (500 MHz, CDCl₃) δ 10.46 (s, 1H), 8.68 (d, 1H, *J* = 2.9 Hz), 8.39 (dd, 1H, *J* = 2.7 and 9.1 Hz), 7.08 (d, 1H, *J* = 9.1 Hz), 4.16 (t, 2H, *J* = 6.2), 1.93 (m, 2H), 1.98 (t, 3H, *J* = 7.37).

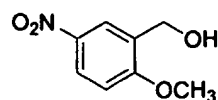
2-hydroxymethyl-4-nitrophenol

A solution of 2-hydroxy-5-nitrobenzaldehyde (5.01 g, 30 mmol) in a mixture of 60 mL 1M NaOH and 30 mL MeOH was cooled to 0 °C. NaBH₄ (1.13 g, 30 mmol) solution in 15 mL 1M NaOH and 5 mL MeOH was added slowly. The reaction mixture was stirred for 24 hours at room temperature. The mixture was poured into ice cooled 2M HCl and extracted with EtOAc. The organic layer was washed, dried, and evaporated *in vacuo* to give the alcohol as a yellow solid (5.1g, 100%): MP (112-114 °C); ¹H NMR (DMSO-*d*₆, 400 MHz) δ 11.08 (s, 1H), 8.18 (d, 1H, *J* = 2.5 Hz), 8.00 (dd, 1H, *J* = 2.5 and 8.7 Hz), 6.92 (d, 1H, *J* = 8.8 Hz), 5.20 (br, 1H), 4.49 (s, 2H).

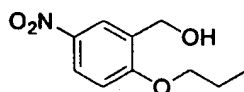
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2-methoxy-5-nitrobenzylalcohol

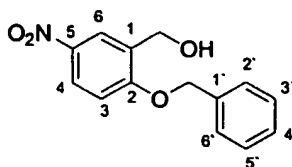
This compound was prepared by reduction of 2-methoxy-5-nitrobenzaldehyde methyl hemiacetal using a method similar to that described for preparing 2-hydroxymethyl-4-nitrophenol in 76% yield: MP 121-122 °C; ¹H NMR (DMSO-*d*₆, 500 MHz) δ 8.22 (d, 1H, *J* = 1.22 Hz), 8.16 (dd, 1H, *J* = 2.7 and 9.1), 7.16 (d, 1H, *J* = 8.9 Hz), 4.50 (s, 2H), 3.90 (s, 3H).

5-nitro-2-propyloxy-benzylalcohol

10

This compound was prepared by reduction of 5-nitro-2-propyloxybenzaldehyde using a method similar to that described for preparing 2-hydroxymethyl-4-nitrophenol in 93% yield: MP (No Sample left for MP); ¹H NMR (400 MHz, DMSO-*d*₆) 8.22 (d, 1H, *J* = 2.6 Hz), 8.13 (dd, 1H, *J* = 2.9 and 9.2 Hz), 7.14 (d, 1H, *J* = 9.2 Hz), 5.41 (t, 1H, *J* = 5.5 Hz), 4.52 (d, 2H, *J* = 5.8 Hz), 4.08 (t, 2H, *J* = 6.2), 1.75 (m, 2H), 0.98 (t, 3H, *J* = 7.6 Hz).

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2-benzyloxy-5-nitrobenzylalcohol

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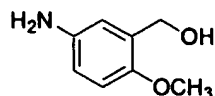
This intermediate was prepared by alkylation of 2-hydroxymethyl-4-nitrophenol with benzyl bromide following the method described for preparation of 2-methoxy-5-nitrobenzaldehyde methyl hemiacetal in a yield of 84%: MP 81-83 °C; ¹H NMR δ (DMSO-*d*₆, 500 MHz) 8.26 (d, 1H, *J* = 2.9 Hz H-6), 8.15 (dd, 1H, *J* = 2.9 and 9.1 Hz, H-4), 7.46 (d, 2H, *J* = 7.0, 2', 6'-Hs) 7.41 (dd, 2H, *J* = 7.0 and 7.7, 3', 5'-

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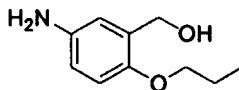
Hs), 7.34 (d, 1H, $J = 7$ Hz, 4'-H), 7.25 (d, 1H, $J = 9.1$ Hz, 3-H), 5.4 (br, 1H, OH), 5.29 (s, 2H, CH₂), 4.57 (s, 2H, CH₂).

3-hydroxymethyl-4-methoxyaniline

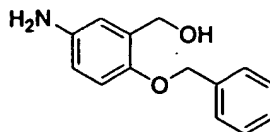
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A mixture of 2-methoxy-5-nitrobenzylalcohol (1.02 g, 6.03 mmol) and SnCl₂·H₂O (6.8 g, 30.15 mmol) in EtOH (20 mL) was heated at 70 °C for 1 hour.

After cooling, the mixture was treated with 2M NaOH and extracted with ether. The organic layer was washed with water, dried, and evaporated under vacuum to provide 10 2.18 g (84%) of the aniline 3-hydroxymethyl-4-methoxyaniline: ¹H NMR (DMSO-*d*₆, 500 MHz) δ 6.66 (d, 1H, $J = 2.2$ Hz), 6.61 (d, 1H, $J = 8.6$ Hz), 6.38 (dd, 1H, $J = 2.4$ and 8.2 Hz), 4.81 (t, 1H, $J = 5.5$ Hz), 4.54 (br, 2H), 4.37 (d, 2H, $J = 5.8$ Hz), 3.61 (s, 3H).

15 3-hydroxymethyl-4-propyloxyaniline

This compound was prepared by reduction of 5-nitro-2-propyloxybenzylalcohol using the method described for the preparation of 3-hydroxymethyl-4-methoxyaniline in 37% yield: ¹H NMR (DMSO-*d*₆, 500 MHz) δ 6.66 (d, 1H, $J = 2.5$ 20 Hz), 6.60 (d, 1H, $J = 8.6$ Hz), 6.35 (dd, 1H, $J = 2.7$ and 8.5 Hz), 4.79 (t, 1H, $J = 5.8$ Hz), 4.54 (br, 2H), 4.37 (d, 2H, $J = 6.1$ Hz), 3.74 (t, 2H, $J = 6.4$ Hz), 1.65 (m, 2H), 0.94 (t, 3H, $J = 7.4$ Hz).

4-benzyloxy-3-hydroxymethylaniline

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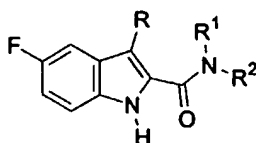
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This compound was prepared by reduction of 2-benzyloxy-5-nitrobenzylalcohol using the method described for preparation of 3-hydroxymethyl-4-methoxyaniline in 86% yield: ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.40 (d, 2H, J = 7.3 Hz), 7.36 (dd, 2H, J = 7.3 and 7.6 Hz), 7.28 (dd, 1H, J = 7.0 and 7.4), 6.70 (d, 1H, J = 8.5 Hz), 6.68 (d, 1H, J = 2.4 Hz), 6.35 (dd, 1H, J = 2.8 and 8.3 Hz), 4.92 (s, 2H), 4.84 (t, 1H, J = 5.8 Hz), 4.59 (br, 2H), 4.44 (d, 2H, J = 6.4 Hz).

B. Formation of Libraries

10 General Structure



$\text{R} = \text{H}, \text{Ph}$

$\text{R}^1, \text{R}^2 = \text{H}, \text{alkyl}, \text{aryl}, \text{aralkyl}, \text{heterocyclic}$

1. General Procedures For Amide Coupling

15 a. Method A

To a cold mixture (at 0 °C) of an amine (see Table VI below for amines) (0.15 mL of 1M solution in CH_2Cl_2 , 0.15 mmol), an acid (5-fluoroindole-2-carboxylic acid or 5-fluoro-3-phenylindole-2-carboxylic acid) (0.15 mmol as 0.15 mL of 1M solution in THF) in CH_2Cl_2 (0.5 mL) was added and cooled to 0 °C. Subsequently, a mixture of 1-(3-dimethylaminopropyl)-3-ethylcarbodiimide (EDCI) (0.15 mmol) and Et_3N (0.06 mmol) in CH_2Cl_2 (0.5 mL) was added and the reaction was shaken in a Bohdan orbital shaker (Mettler-Toledo Bohdan, Vernon Hills, IL) at 0 °C for 30 minutes then at room temperature for 18 hours. After adding 0.5 mL of CH_2Cl_2 and 0.5 mL MeOH, the mixture was passed through a cartridge charged with a cationic exchange resin (Dowex 50wX4-200, Aldrich Chemical Co., Milwaukee, WI, pre-washed with 1M HCl, H_2O , H_2O -MeOH, MeOH, MeOH- CH_2Cl_2). The eluent was directly passed through a chromatography cartridge containing silica gel mixed with 10% Na_2CO_3 .

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The product was eluted with 2 mL CH₂Cl₂-MeOH (2 mL), CH₂Cl₂ (2 mL), and CH₂Cl₂-MeOH (2 mL). The fraction(s) containing pure product was identified by TLC (EtOAc-Hexane, 1:1). The compounds were characterized and their relative purity was estimated using ¹H NMR.

5

b. Method B

A mixture of an amine (see Table VI below for amines) (0.1 mmol), an acid (5-fluoroindole-2-carboxylic acid or 5-fluoro-3-phenylindole-2-carboxylic acid) (0.1 mmol as 0.1 mL of 1M solution in DMF), and diisopropylethylamine (DIEA) (0.05 mL, 0.3 mmol) was cooled to 0 °C. (benzotriazol-1-yloxy)tripyrrolidino-phosphonium-hexafluorophosphate (PyBOP) (0.1 mmol as 0.1 mL of 1M solution in DMF) was added. The reaction mixture was shaken using an orbital shaker at 0 °C for 30 minutes then at room temperature for 18 hours. EtOAc was added to the mixture and the organic solution was washed with 1M HCl (2x1 mL), brine (1 mL) NaHCO₃ (2x1 mL), and brine (1 mL). The organic layer was passed through a silica gel cartridge containing a top layer of anhydrous MgSO₄ and moistened with hexane. The product amide was eluted with hexane (1x1 mL), hexane-EtOAc 2:1 (3x1 mL), hexane-EtOAc 1:1 (2x2 mL), and hexane-EtOAc 1:2 (1x2 mL). The fraction(s) containing pure product was identified by TLC (EtOAc-hexane 1:1 and EtOAc-hexane 1:2 in the case of 5-fluoro-3-phenylindole-2-carboxylic acid amide derivatives). The compounds were characterized and their relative purity was estimated using ¹H NMR.

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20

c. Method C

A mixture of an amine (see Table VI below for amines) (0.1 mmol), an acid (5-fluoroindole-2-carboxylic acid or 5-fluoro-3-phenylindole-2-carboxylic acid) (0.1 mmol as 0.1 mL of 1M solution in THF), and DIEA (0.05 mL, 0.3 mmol) in 0.4 mL of CH₂Cl₂-THF (3:1) was cooled to 0 °C. PyBrOP (0.1 mmol) was added. The reaction mixture was shaken using an orbital shaker at 0 °C for 30 minutes then at room temperature for 48 hours (0.1 mL THF and 0.2 mL CH₂Cl₂ were added after 24 hours). EtOAc was added to the mixture and the organic solution was washed with 1M HCl (2x1 mL), brine (1 mL) NaHCO₃ (2x1 mL), and brine (1 mL). The organic

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layer was passed through a silica gel cartridge containing a top layer of anhydrous MgSO_4 and moistened with hexane. The product amide was eluted with hexane (1x1 mL), hexane-EtOAc 2:1 (3x1 mL), hexane-EtOAc 1:1 (2x2 mL), and hexane-EtOAc 1:2 (1x2 mL). The fraction(s) containing pure product was identified by TLC (EtOAc-hexane 1:1 and EtOAc-hexane 1:2 in the case of 5-fluoro-3-phenylindole-2-carboxylic acid amide derivatives). The compounds were characterized by ^1H NMR.

d. Method D

10 Preparation of 5-fluoroindole-2-carboxylic acid chloride

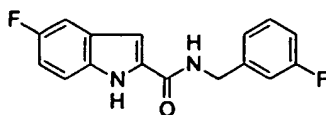
5-fluoroindole-2-carboxylic acid (537 mg, 3 mmol) was dissolved in DME (8 mL). 0.6 mL triethylamine was added and the mixture cooled to 0 °C. Thionyl chloride (0.44 mL, 6 mmol) mixed with 4 mL DME was added cautiously using addition funnel over 10 minutes while stirring. The mixture was left to stir for 30 minutes. The formed precipitate was filtered off, and the solvent was evaporated under reduced pressure to give yellow solid of the acid chloride.

Reaction of amines with 5-fluoroindole-2-carboxylic acid chloride

A mixture of an amine (see Table VI below for amines) (1 mmol) and pyridine (0.18 mL) in 1 mL DCM was cooled to 0 °C. 5-fluoroindole-2-carboxylic acid chloride (19.8 mg, 1 mmol) was added, then reaction was stirred at room temperature for 1 hour. The resulting amide (in DCM) was washed with 1M HCl, then with Brine. The crude product was purified by silica gel chromatography.

25 e. Representative Examples of Amide Coupling Methods

Synthesis of Compound 1z



30 To a mixture of 3-fluorobenzylamine (2.03 g, 20 mmol) and 5-fluoroindole-2-carboxylic acid (3.58g, 20 mmol) in DMF (50 mL), was added a solution of DIEA

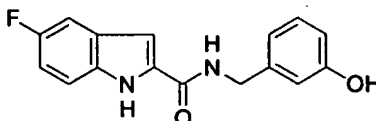
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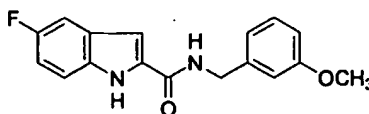
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(6.98 mL, 40 mmol) in 15 mL CH₂Cl₂. The mixture was cooled to 0 °C and PyBOP (10.41 g, 20 mmol) was added portion wise. The reaction mixture was stirred at 0 °C for 30 minutes, then at room temperature for 4 hours. EtOAc (400 mL) was added to the mixture and the organic solution was washed with 2M HCl (4x200 mL), brine (200 mL), NaHCO₃ (4x200 mL), and brine (2x200 mL). The organic layer was dried (MgSO₄) and concentrated *in vacuo* to furnish the crude product as off-white solid. Recrystallization from MeOH and CH₂Cl₂ provided 5.36 g (93%) of **1z** as white crystals: MP 239-241 °C; ¹H NMR (DMSO-*d*₆, 500 MHz) δ 11.73 (s, 1H), 9.12 (t, 1H, *J* = 6.1 Hz), 7.39 (complex, 3H), 7.17 (complex, 2H), 7.07 (dd, 1H, *J* = 2.2 and 9.5 Hz), 7.07 (dd, 1H, *J* = 2.2 and 9.0 Hz), 7.03 (ddd, 1H, *J* = 2.4, 9.1 and 9.2 Hz), 4.52 (d, 2H, *J* = 6.1 Hz); Anal. (C₁₆H₁₂F₂N₂O) C, 67.13; H, 4.23; N, 9.79; Found; C, 66.91; H, 4.31; N, 9.81.

Synthesis of Compound 1a



(a) Preparation of Methoxy Intermediate



Following same procedure mentioned above for the synthesis of **1z**, this compound was prepared starting from 20 mmol of amine and acid. Purification with flash column chromatography afforded 5.43 g (91%) of the methoxy intermediate as off-white crystalline solid: MP 192 °C.

(b) Demethylation

A mixture of the methoxy intermediate (5 g, 16.7 mmol) and CH₂Cl₂ (80 mL) was placed in a multi neck flask equipped with a dropping funnel and a thermometer. The flask was cooled to 0°C in an ice/salt bath. A solution of BBr₃ in CH₂Cl₂ (80 mL) was added dropwise while keeping the temperature less than 5 °C. The mixture was

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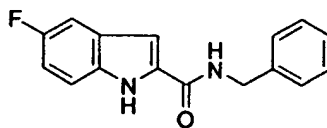
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stirred at room temperature for 3 hours. After addition of ice and 3M HCl (200 mL), the mixture was left to stir overnight. The precipitated solid product was collected by filtration, washed with water, and dried. Crystallization from CH₂Cl₂ and MeOH furnished 4.2 g (88%) of compound 1a: MP 213 °C; ¹H NMR (DMSO-*d*₆, 400 MHz) δ 11.68 (br, 1H), 9.31 (br, 1H), 9.01 (t, 1H, *J* = 6.0 Hz), 7.39 (complex, 2H), 7.14 (s, 1H), 7.09 (dd, 1H, *J* = 8.0 and 7.7 Hz), 7.02 (ddd, 1H, *J* = 9.2, 8.9 and 2.5 Hz), 6.72 (d, 2H, *J* = 7.3 Hz), 6.61 (d, 1H, *J* = 8.4 Hz), 4.41 (d, 2H, *J* = 5.9 Hz), HRMS (EI): Required M⁺ for C₁₆H₁₃FN₂O₂, 284.0956; Found, 284.0960; Anal. (C₁₆H₁₃FN₂O₂) C, 67.60; H, 4.61; F, N, 9.85; Found C, 67.50; H, 4.65; F, N, 9.76.

f. Other Representative Compounds Obtained and Relative Purity Data

The following are examples of compounds obtained using the above methods and their relative purity data. Table VI, below, lists all compounds obtained.

Compound 1bb

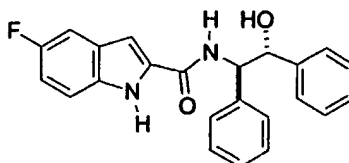


¹H NMR (acetone-*d*₆, 400 MHz) δ 10.85 (br, 1H), 8.29 (br, 1H), 7.53 (dd, 1H, *J* = 9.9 and 4.6 Hz), 7.36 (d, 1H, *J* = 7.4), 7.30 (complex, 3H), 7.22 (dd, 1H, *J* = 7.3 and 7.0 Hz), 7.12 (s, 1H), 7.02 (ddd, 1H, *J* = 2.6 and 9.2 and 9.1), 4.60 (d, 2H, *J* = 6.3 Hz).

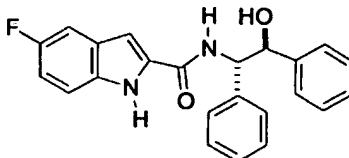
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Compound 1cc

- ¹H NMR (Acetone-*d*₆, 500 MHz) δ 10.74 (br, 2H) 8.01 (d, br, 1H, *J* = 9.0 Hz), 7.45
5 (dd, 1H, *J* = 9.0 and 4.6 Hz), 7.37 (d, 2H, *J* = 7.4 Hz), 7.34 (d, 2H, *J* = 7.4 Hz), 7.28
(dd, 1H, *J* = 9.5 and 2.5 Hz), 7.24 to 7.10 (complex. m, 7H), 6.99 (ddd, 1H, *J* = 9.3,
9.2 and 2.6 Hz), 5.40 (dd, 1H, *J* = 9.0 and 6.4 Hz), 5.20 (dd, 1H, *J* = 6.2 and 4.6 Hz),
4.71 (d, 1H, *J* = 4.6 Hz); LRMS (EI), *m/z* 356.1 (*M*⁺-H₂O).

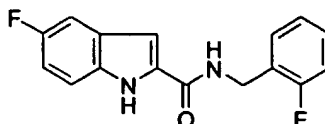
10 Compound 1dd

- ¹H NMR (Acetone-*d*₆, 500 MHz) δ 10.80 (br, 2H) 8.04 (d, br, 1H, *J* = 8.7 Hz), 7.43
15 (dd, 1H, *J* = 9.0 and 4.8 Hz), 7.38 (dd, 2H, *J* = 8.0 and 1.4 Hz), 7.34 (dd, 2H, *J* = 8.0
and 1.4 Hz), 7.28 (dd, 1H, *J* = 9.6 and 2.4 Hz), 7.25 to 7.11 (complex. m, 7H), 6.98
(ddd, 1H, *J* = 9.2, 9.1 and 2.5 Hz), 5.41 (dd, 1H, *J* = 8.8 and 6.6 Hz), 5.21 (dd, 1H, *J* =
6.2 and 4.8 Hz), 4.71 (d, 1H, *J* = 4.6 Hz).

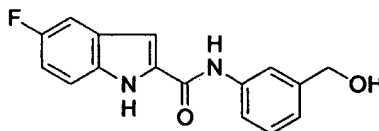
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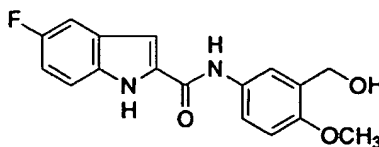
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Compound 1bbb

¹H NMR (acetone-*d*₆, 500 MHz) δ 10.89 (br, 1H), 8.31 (br, 1H), 7.54 (dd, 1H, *J* = 9.1 and 4.6 Hz), 7.45 (dd, 1H, *J* = 7.7 and 7.7 Hz), 7.29 (complex, 2H), 7.17-7.08
5 (complex, 3H), 7.03 (ddd, 1H, *J* = 9.2, 9.1 and 2.6 Hz), 4.66 (d, 2H, *J* = 5.8 Hz).

Compound 1yyy

¹H NMR (Acetone-*d*₆, 500 MHz) δ 10.99 (br, 1H), 9.57 (br, 1H), 7.80 (s, 1H), 7.76 (d,
10 1H, *J* = 8.3 MHz), 7.57 (dd, 1H, *J* = 9.0 and 4.4 Hz), 7.35 (dd, 1H, 9.2 and 2.4 Hz),
3.34 (s, 1H), 7.29 (dd, 1H, *J* = 7.7 and 7.8 Hz), 7.09 (d, 1H, *J* = 8.8 Hz), 7.06 (ddd,
1H, *J* = 9.2, 8.9 and 2.4 Hz), 4.63 (d, 2H, *J* = 5.8 Hz), 4.24 (t, 1H, *J* = 5.8 Hz);
LRMS (EI) *m/z* 284.1 (74%, M⁺).

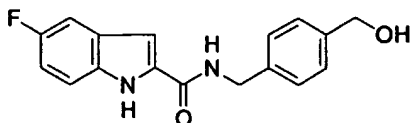
15 Compound 1ccc

¹H NMR (acetone-*d*₆, 500 MHz) δ 10.96 (br, 1H), 9.49 (br, 1H), 7.79 (complex, 2H),
7.56 (dd, 1H, *J* = 8.9 and 4.5 Hz), 7.34 (complex, 2H), 7.05 (ddd, 1H, *J* = 9.2, 9.1 and
20 2.4 Hz), 6.92 (d, 1H, *J* = 8.6 Hz), 4.65 (d, 1H, *J* = 7.0 Hz), 4.06 (t, 1H, *J* = 5.8), 3.81
(s, 1H); LRMS (EI) *m/z* 314.12 (51%, M⁺).

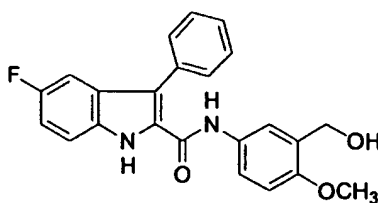
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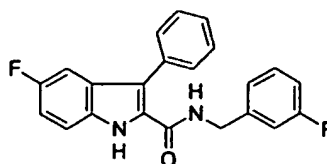
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Compound 1o

- 5 ^1H NMR (acetone- d_6 , 500 MHz) δ 10.94 (br, 1H), 8.31 (br, 1H), 7.52 (dd, 1H, J = 8.9 and 4.6), 7.33 (d, 2H, J = 8.9), 7.30 (d, 2H, J = 8.5), 7.29 (dd, 1H, J = 9.6 and 2.6 Hz), 7.13 (s, 1H), 7.02 (ddd, 1H, J = 9.3, 9.1 and 2.4 Hz), 4.60 (d, 4H, J = 5.8 Hz), 4.15 (t, 1H, J = 5.8 Hz); LRMS (EI) m/z 298.12 (100%, M^+).

10 Compound 2f

- ^1H NMR (acetone- d_6 , 500 MHz) δ 11.12 (br, 1H), 8.07 (br, 1H), 7.66-7.60 (m, complex, 5H), 7.52 (m, 1H), 7.36 (d, 1H, J = 2.2 Hz), 7.30 (dd, 1H, J = 8.7 and 2.6),
15 7.15-7.09 (m, complex, 2H), 6.84 (d, 1H, J = 8.8 Hz), 4.56 (d, 2H, J = 6.1 Hz), 4.04 (t, 1H, J = 5.8 Hz), 3.77 (s, 3H).

Compound 2g

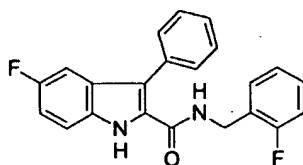
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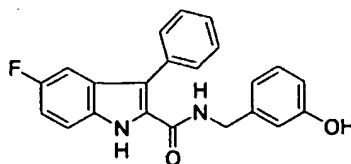
¹H NMR (Acetone-*d*₆, 500 MHz) δ 11.02 (br, 1H), 7.59 (dd, 1H, *J* = 9.7 and 4.6 Hz), 7.53 (d, 1H, *J* = 9.8 Hz), 7.47 (dd, 2H, *J* = 7.9 and 7.4 Hz), 7.40 (m, 1H), 7.31 (dd, 1H, *J* = 7.0 and 6.5 Hz), 7.08 (complex, 2H), 7.03 (d, 1H, *J* = 7.7 Hz), 6.99 (complex, 2H), 6.91 (br, 1H), 4.48 (d, 2H, *J* = 5.8 Hz); LRMS (EI) *m/z* 362.14 (85%, M⁺).

5

Compound 2s

¹H NMR (Acetone-*d*₆, 500 MHz) δ 11.03 (br, 1H), 7.57-7.45 (complex, 4H), 7.544 (m, 1H), 7.31-7.24 (complex, 2H), 7.13-7.055 (complex, 4H), 6.76 (br, 1H), 4.50 (d, 2H, *J* = 5.2 Hz); LRMS (EI) *m/z* 362.1 (95%, M⁺).

10

Compound 3q

15

¹H NMR (Acetone-*d*₆, 500 MHz) δ 10.99 (br, 1H), 8.26 (s, 1H), 7.58 (dd, 1H, *J* = 9.5 and 4.6 Hz), 7.51 (dd, 2H, *J* = 8.2 and 1.4 Hz), 7.46 (dd, 2H, *J* = 7.7 and 7.3 Hz), 7.38 (m, 1H), 7.10-7.05 (complex, 3H), 6.72 (br, 1H), 6.67 (complex, 2H), 6.62 (d, 1H, *J* = 7.6 Hz), 4.38 (d, 2H, *J* = 6.2 Hz); LRMS (EI) *m/z* 360.12 (100%, M⁺).

20

2. General Procedure For Oxidation Of Benzyl Alcohol Amide Derivatives To Benzaldehyde: Preparation Of Compounds 3b, 3d, 3e, 3f, 3g, and 3h

The starting benzyl alcohol amide derivative was dissolved in a 1:1 mixture of CH₂Cl₂ and THF (5 mL/mmol), pyridinium chlorochromate (2 molar equivalent) was

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added, and the mixture was stirred at room temperature for 3.5 hours. EtOAc and water were added. The brown solid was removed by filtration. The organic phase was washed several times with NaHCO₃, brine, dried, and concentrated. Product aldehyde was purified by crystallization and confirmed by ¹H NMR (disappearance of the methylene of benzyl alcohol and appearance of aldehyde peak).

5

The following table sets forth the structures made by the above methods:

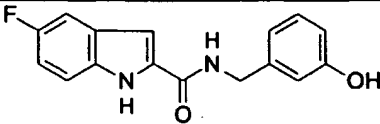
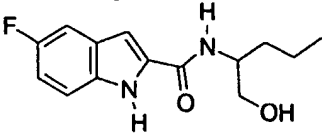
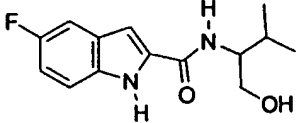
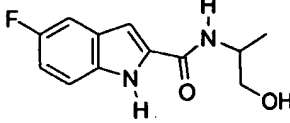
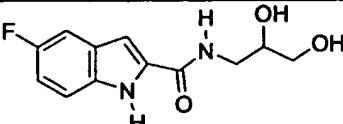
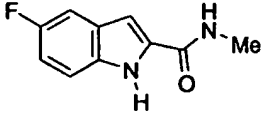
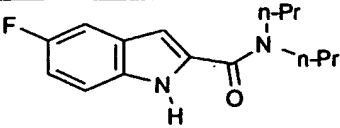
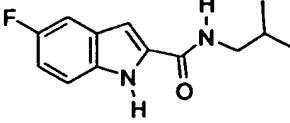
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TABLE VI

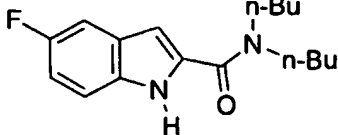
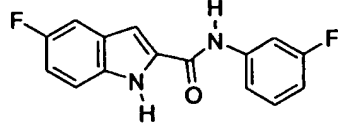
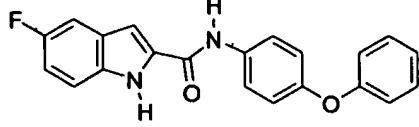
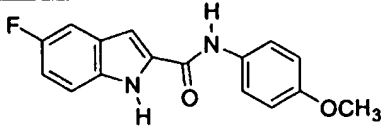
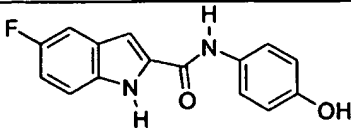
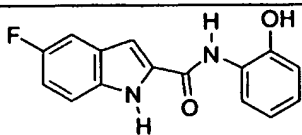
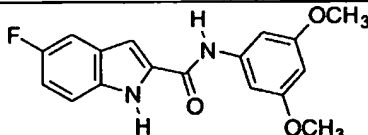
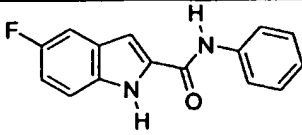
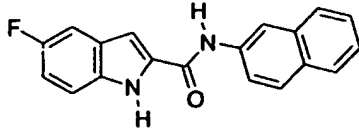
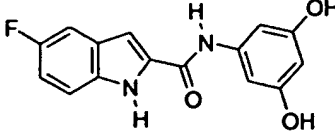
LIBRARY OF 5-FLUOROINDOLE-2-CARBAXAMIDE
COMPOUNDS AND METHOD OF PREPARATION

Cmpd Code	Structure	M.Wt.	Method of Preparation
1a		284.29	See Example 1
1b		264.3	Amide Coupling Method A
1c		264.3	Amide Coupling Method A
1d		236.24	Amide Coupling Method A
1e		252.24	Amide Coupling Method A
1f		192.19	Amide Coupling Method A
1g		262.32	Amide Coupling Method A
1h		234.27	Amide Coupling Method A

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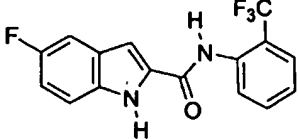
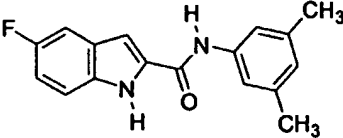
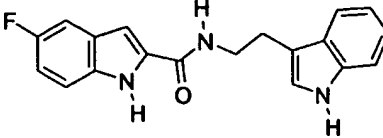
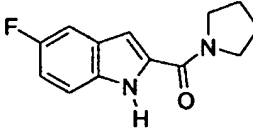
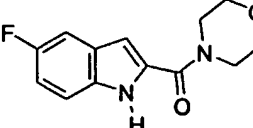
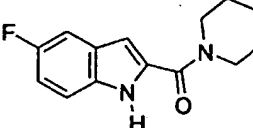
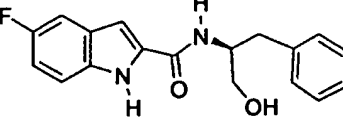
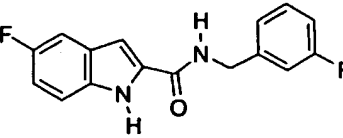
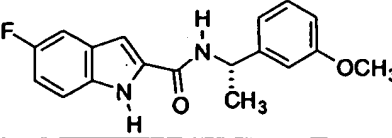
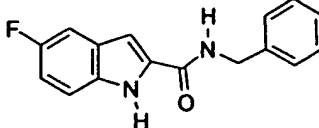
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1i		290.38	Amide Coupling Method A
1j		272.25	Amide Coupling Method A
1k		346.35	Amide Coupling Method A
1l		284.29	Amide Coupling Method A
1m		270.26	Amide Coupling Method A
1n		270.26	Amide Coupling Method A
1o		314.31	Amide Coupling Method A
1p		254.26	Amide Coupling Method A
1q		304.32	Amide Coupling Method A
1r		286.26	Amide Coupling Method A

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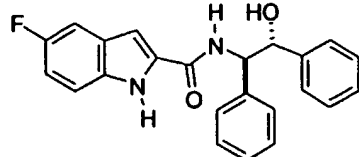
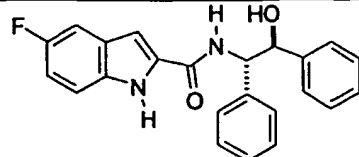
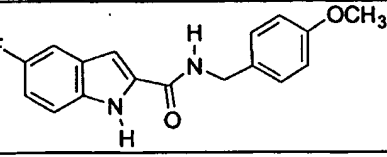
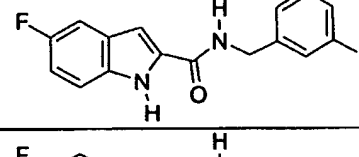
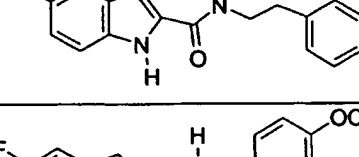
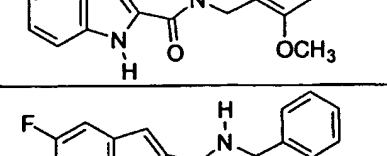
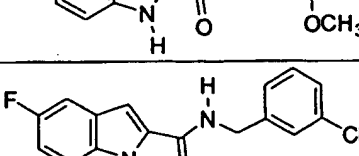
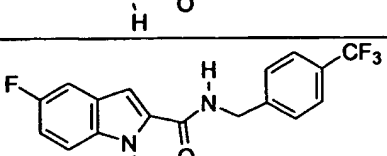
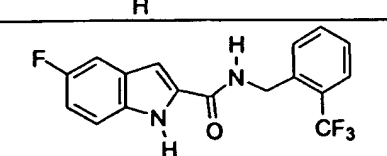

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1s		322.26	Amide Coupling Method A
1t		282.31	Amide Coupling Method A
1u		321.35	Amide Coupling Method A
1v		232.25	Amide Coupling Method A
1w		248.25	Amide Coupling Method A
1x		246.28	Amide Coupling Method A
1y		312.34	Amide Coupling Method A
1z		286.28	Amide Coupling Method A
1aa		312.34	Amide Coupling Method A
1bb		268.29	Amide Coupling Method A

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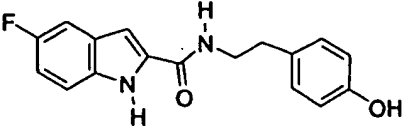
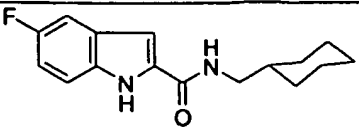
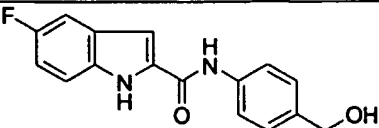
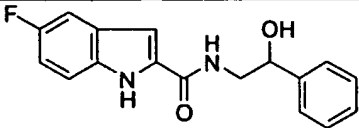
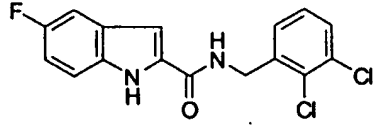
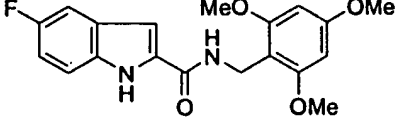
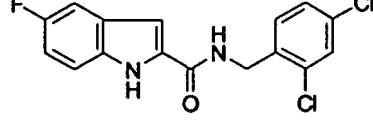
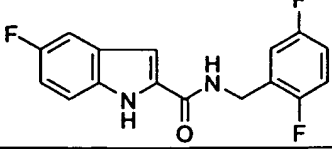
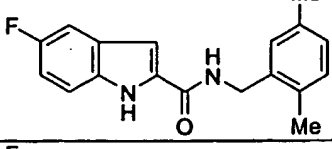
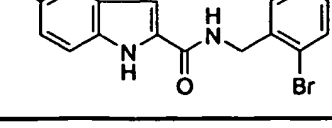
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1cc		374.41	Amide Coupling Method A
1dd		374.41	Amide Coupling Method A
1ee		298.31	Amide Coupling Method A
1ff		394.18	Amide Coupling Method A
1gg		282.31	Amide Coupling Method A
1hh		328.34	Amide Coupling Method A
1ii		298.31	Amide Coupling Method A
1jj		336.28	Amide Coupling Method A
1kk		336.28	Amide Coupling Method A
1ll		336.28	Amide Coupling Method A

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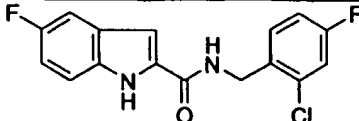
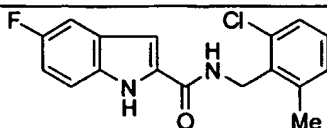
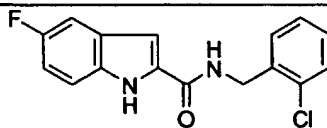
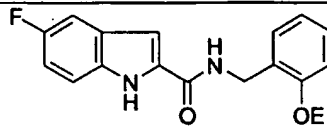
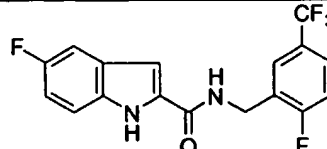
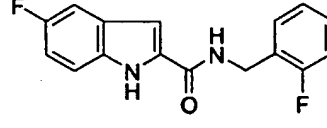
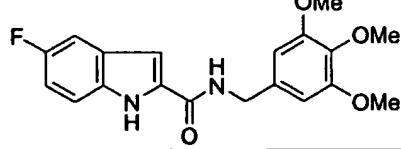
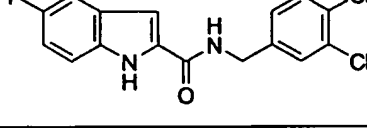
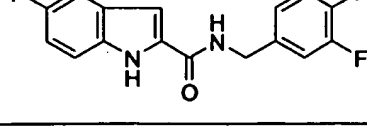
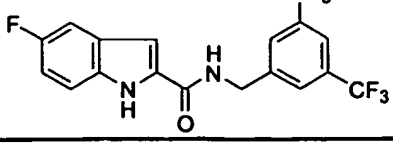
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1nn		274.33	Amide Coupling Method A
1oo		284.29	Amide Coupling Method A
1pp		298.31	Amide Coupling Method A
1qq		337.18	Amide Coupling Method A
1rr		358.36	Amide Coupling Method A
1ss		337.18	Amide Coupling Method A
1tt		304.27	Amide Coupling Method A
1uu		296.34	Amide Coupling Method A
1vv		347.18	Amide Coupling Method A

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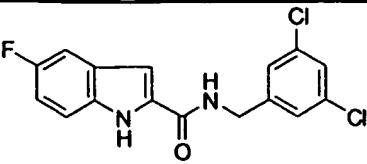
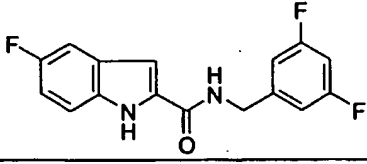
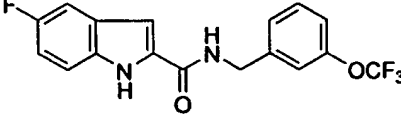
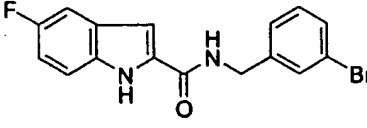
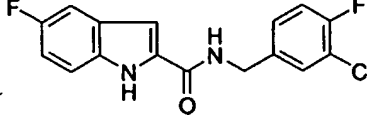
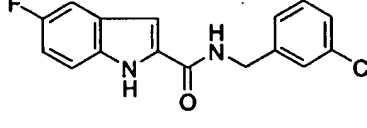
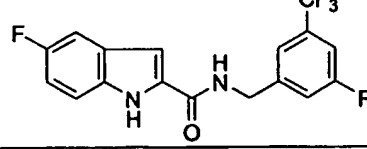
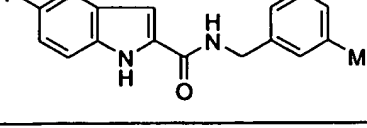
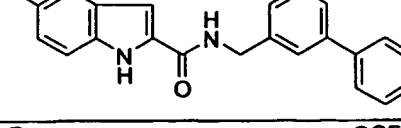
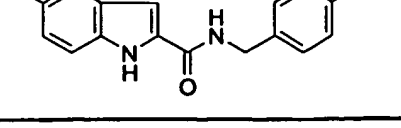
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1ww		320.72	Amide Coupling Method A
1xx		316.76	Amide Coupling Method A
1yy		302.73	Amide Coupling Method A
1zz		312.34	Amide Coupling Method A
1aaa		354.27	Amide Coupling Method A
1bbb		286.28	Amide Coupling Method A
1ccc		358.36	Amide Coupling Method A
1ddd		337.18	Amide Coupling Method A
1eee		304.27	Amide Coupling Method A
1fff		404.28	Amide Coupling Method A

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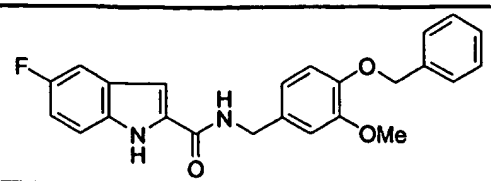
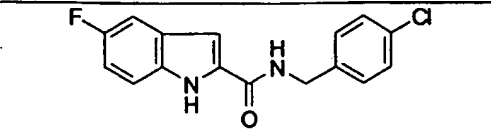
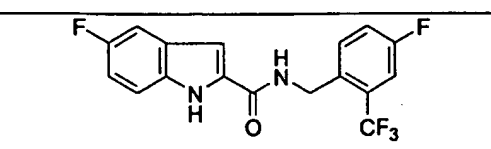
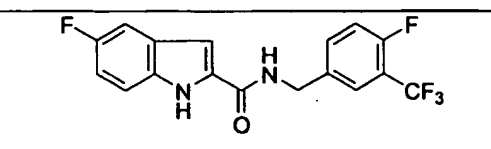
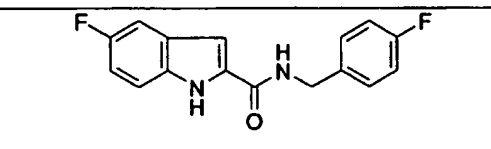
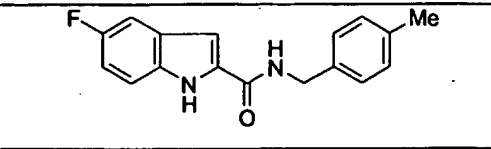
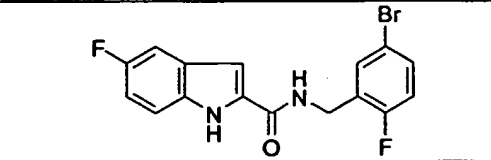
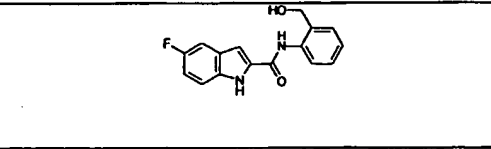
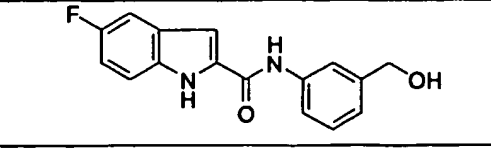
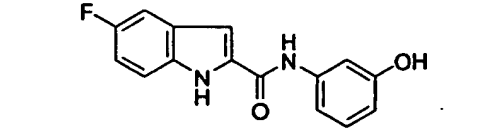
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1hhh		304.27	Amide Coupling Method A
1iii		352.28	Amide Coupling Method A
1jjj		347.18	Amide Coupling Method A
1kkk		320.72	Amide Coupling Method A
1lll		302.73	Amide Coupling Method A
1mmm		354.27	Amide Coupling Method A
1nnn		282.31	Amide Coupling Method A
1ooo		344.38	Amide Coupling Method A
1ppp		352.28	Amide Coupling Method A

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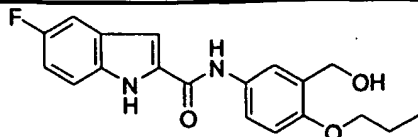
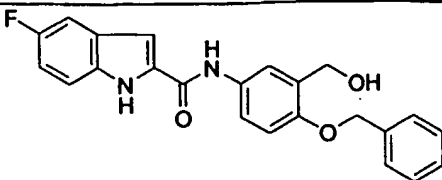
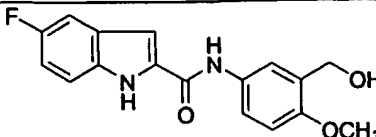
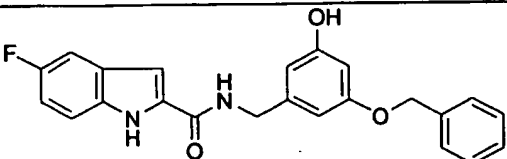
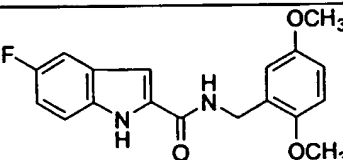
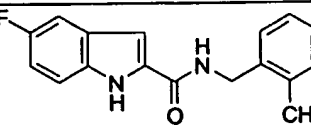
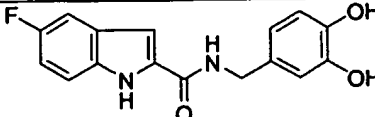
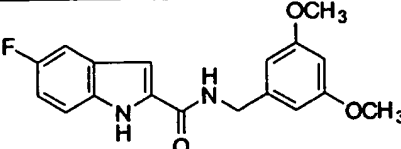
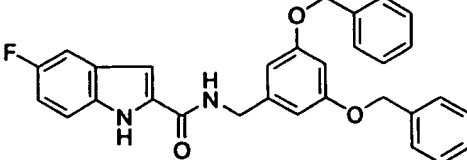
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1qqq		404.43	Amide Coupling Method A
1rrr		302.73	Amide Coupling Method A
1sss		354.27	Amide Coupling Method A
1ttt		354.27	Amide Coupling Method A
1uuu		286.28	Amide Coupling Method A
1vvv		282.31	Amide Coupling Method A
1www		365.17	Amide Coupling Method A
1xxx		284.29	Amide Coupling Method C
1yyy		284.29	Amide Coupling Method B
1zzz		270.26	Amide Coupling Method C

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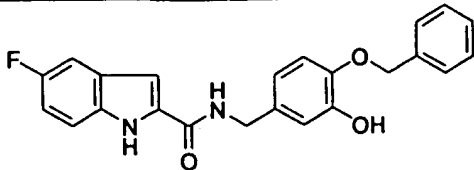
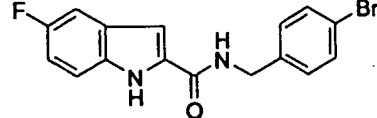
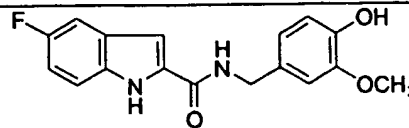
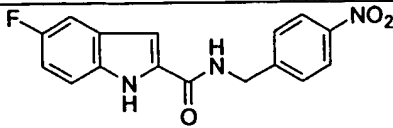
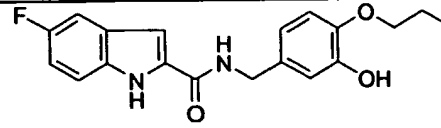
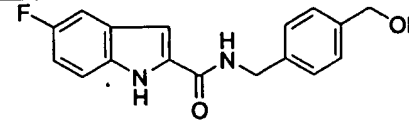
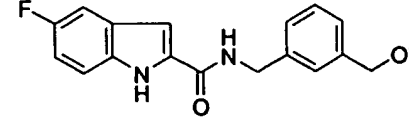
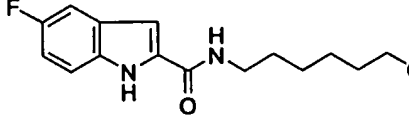
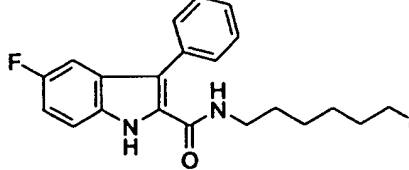
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1aaaa		342.36	Amide Coupling Method C
1bbbb		390.41	Amide Coupling Method C
1cccc		314.31	Amide Coupling Method C
1dddd		390.41	Amide Coupling Method B
1eeee		328.34	Amide Coupling Method B
1ffff		282.31	Amide Coupling Method B
1gggg		300.28	Amide Coupling Method B
1hhhh		328.34	Amide Coupling Method B
1iiii		480.53	Amide Coupling Method B

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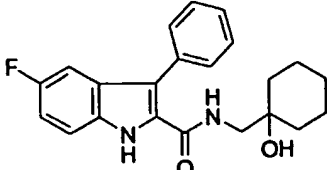
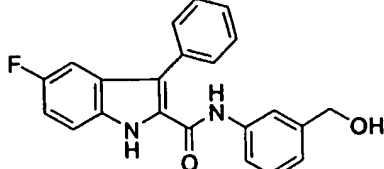
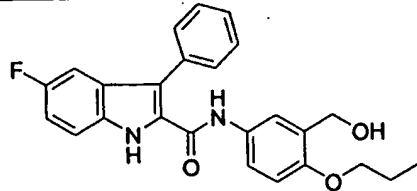
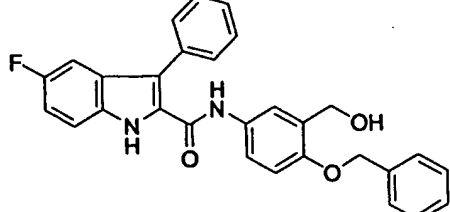
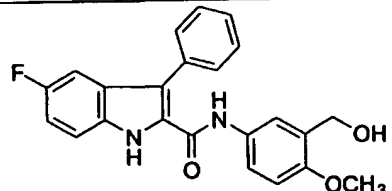
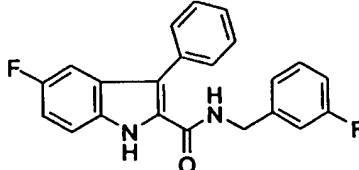
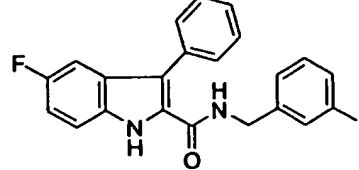
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1kkkk		347.18	Amide Coupling Method B
1lll		314.31	Amide Coupling Method B
1mmm		313.28	Amide Coupling Method B
1nnnn		342.36	Amide Coupling Method B
1oooo		298.31	Amide Coupling Method B
1pppp		298.31	Amide Coupling Method B
1qqqq		278.32	Amide Coupling Method B
2a		354.42	Amide Coupling Method B

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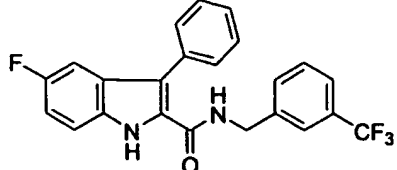
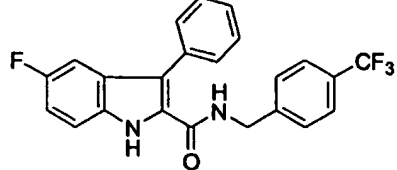
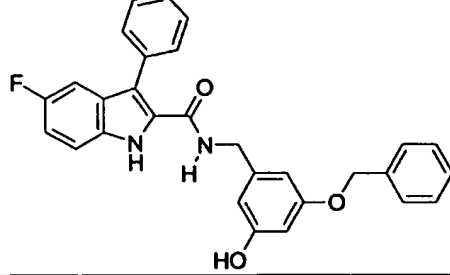
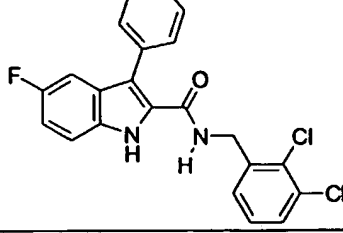
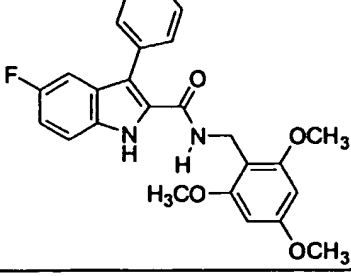
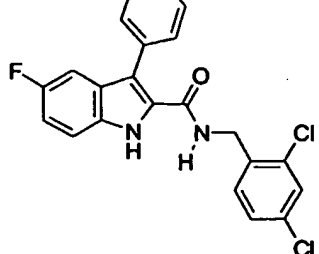
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2b		366.43	Amide Coupling Method B
2c		360.38	Amide Coupling Method B
2d		418.46	Amide Coupling Method B
2e		466.5	Amide Coupling Method B
2f		390.41	Amide Coupling Method B
2g		362.37	Amide Coupling Method B
2h		470.28	Amide Coupling Method B

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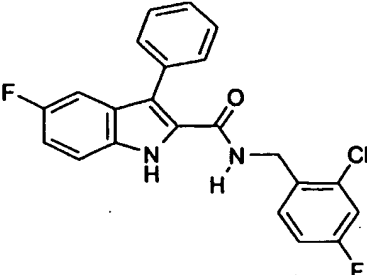
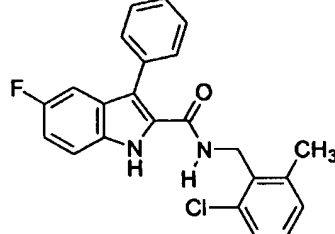
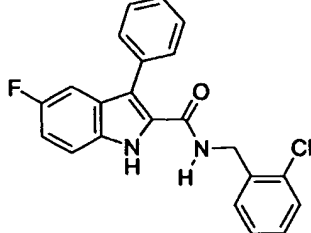
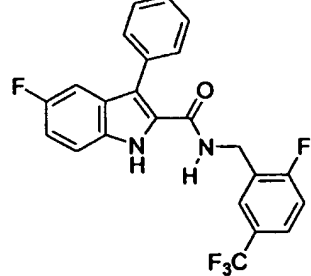
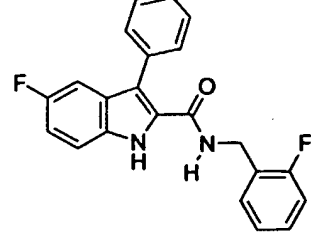
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2i		412.38	Amide Coupling Method B
2j		412.38	Amide Coupling Method B
2k		466.5	Amide Coupling Method B
2l		413.27	Amide Coupling Method B
2m		434.46	Amide Coupling Method B
2n		413.27	Amide Coupling Method B

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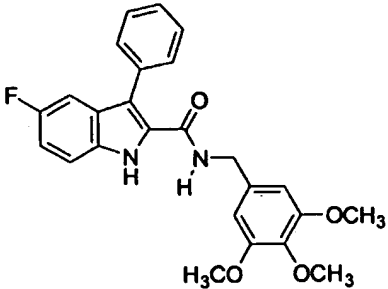
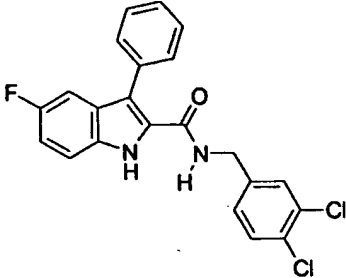
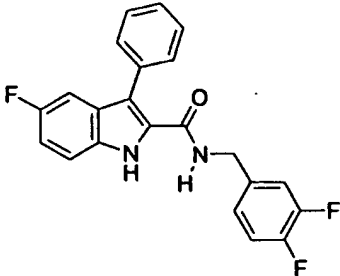
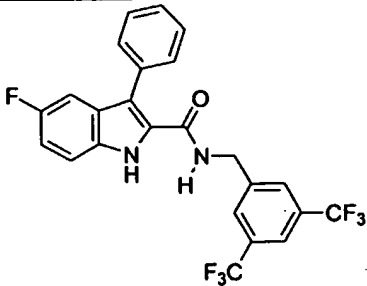
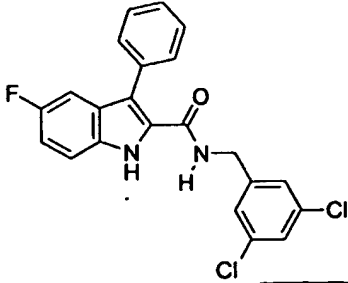
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2o		396.82	Amide Coupling Method B
2p		392.85	Amide Coupling Method B
2q		378.83	Amide Coupling Method B
2r		430.37	Amide Coupling Method B
2s		362.37	Amide Coupling Method B

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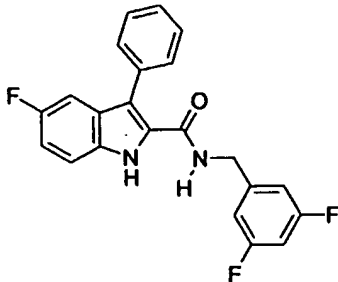
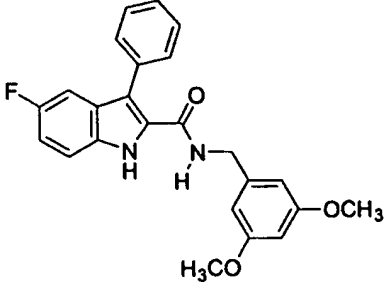
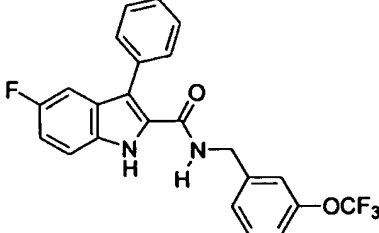
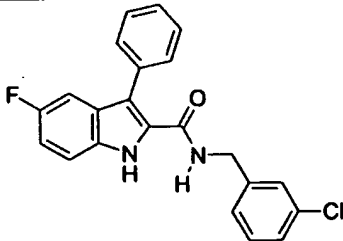
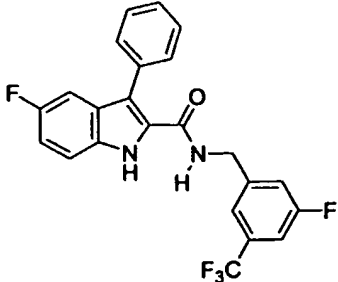
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2t		434.46	Amide Coupling Method B
2u		413.27	Amide Coupling Method B
2v		380.36	Amide Coupling Method B
2w		480.38	Amide Coupling Method B
2x		413.27	Amide Coupling Method B

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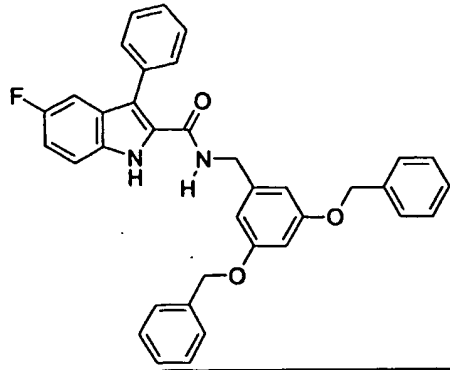
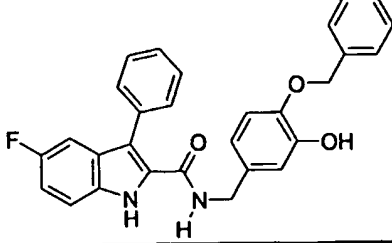
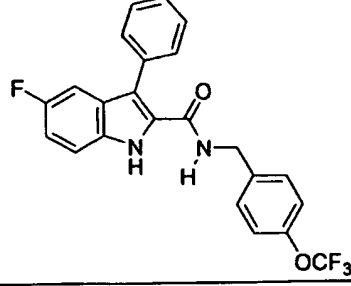
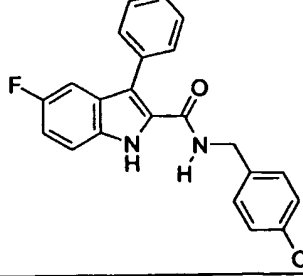
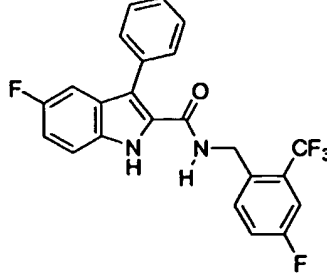
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2y		380.36	Amide Coupling Method B
2z		404.43	Amide Coupling Method B
2aa		428.38	Amide Coupling Method B
2bb		378.83	Amide Coupling Method B
2cc		430.37	Amide Coupling Method B

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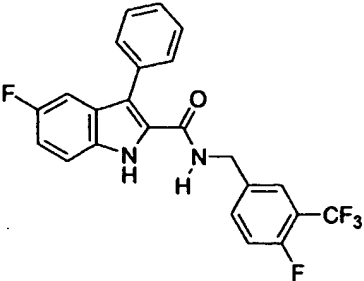
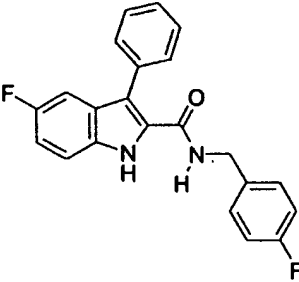
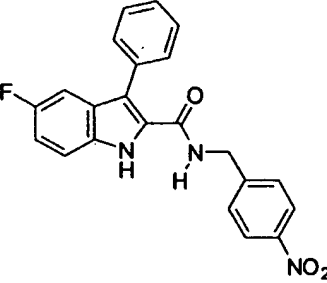
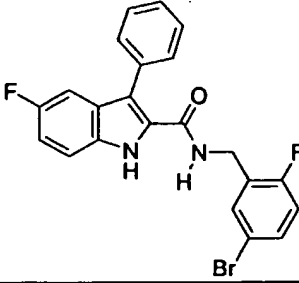
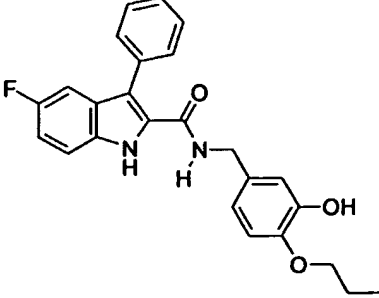
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2dd		556.63	Amide Coupling Method B
2ee		466.5	Amide Coupling Method B
2ff		428.38	Amide Coupling Method B
2gg		378.83	Amide Coupling Method B
2hh		430.37	Amide Coupling Method B

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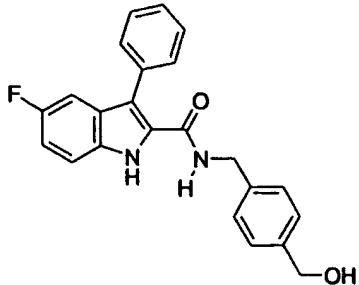
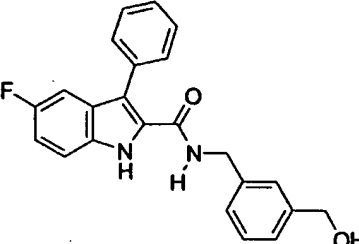
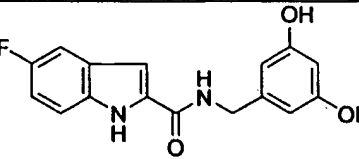
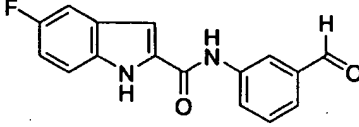
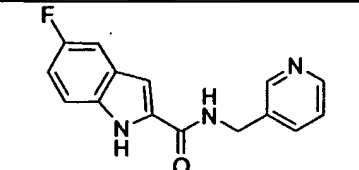
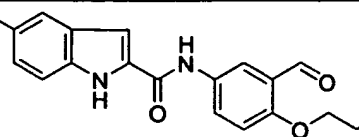
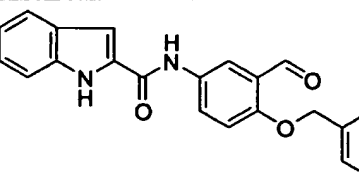
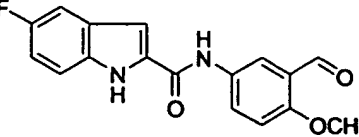
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2ii		431.37	Amide Coupling Method B
2jj		362.37	Amide Coupling Method B
2kk		389.38	Amide Coupling Method B
2ll		441.27	Amide Coupling Method B
2mm		418.46	Amide Coupling Method B

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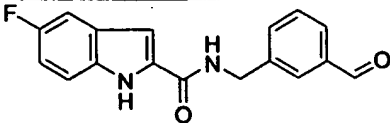
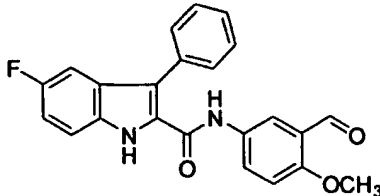
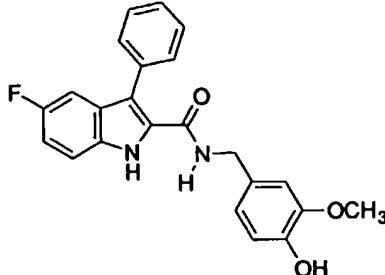
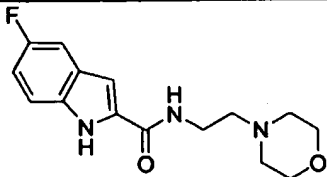
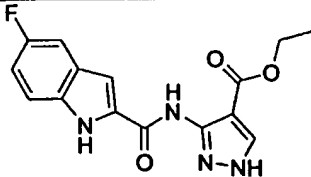
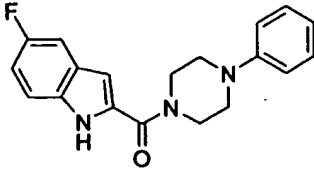
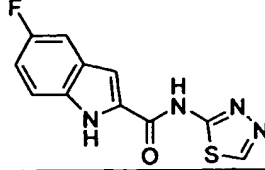
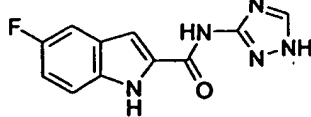
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2nn		374.41	Amide Coupling Method B
2oo		375.41	Amide Coupling Method B
3a		300.28	Demethylation of compound 1hh using BBr ₃ method in Example 1.
3b		282.27	Oxidation of 1yyy
3c		269.29	Amide Coupling Method C
3d		340.35	Oxidation of 1aaaa
3e		388.39	Oxidation of 1bbbb
3f		312.3	Oxidation of 1cccc

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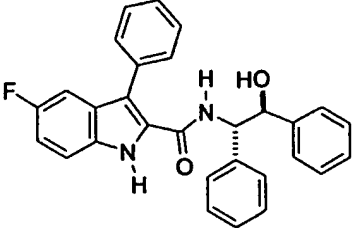
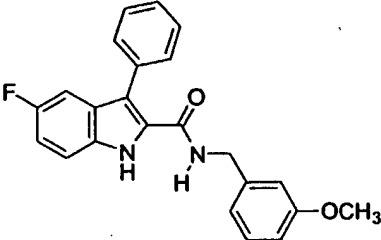
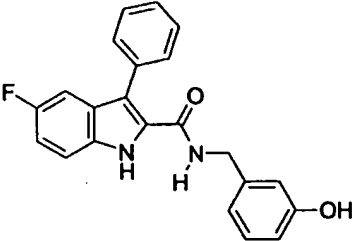
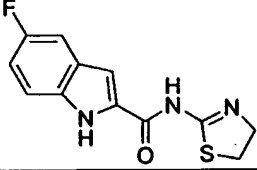
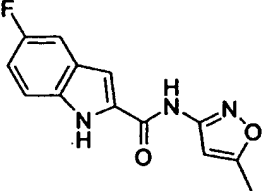
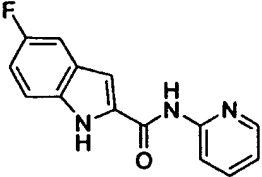
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3g		296.3	Oxidation of 1pppp
3h		388.39	Oxidation of 2f
3i		390.41	Amide Coupling Method B
3j		291.31	Amide Coupling Method C
3k		316.28	Amide Coupling Method C
3l		323.35	Amide Coupling Method C
3m		262.26	Amide Coupling Method C
3n		245.21	Amide Coupling Method C

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3o		450.5	Amide Coupling Method B
3p		374.41	Amide Coupling Method B
3q		360.38	See synthesis of 1a in Example 1
3r		263.3	Amide Coupling Method D
3s		259.24	Amide Coupling Method D
3t		255.25	Amide Coupling Method D

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C. Inhibition of Human Cancer Cell Line H460 and Isolated Src.

Subsequent to synthesis, several of the above compounds were tested for the inhibition of the growth of human lung cancer cell line H460 and the inhibition of isolated Src. To test for inhibition of H460, the cells were seeded at 600 cells/well in 96 well plates in complete medium-RPMI-1640 containing 5% FCS, 5% NuSerum IV, 2 mM L-glutamine, and 10 mM HEPES. Following an overnight incubation, compounds which were solubilized in DMSO and diluted in RPMI-1640, were added to cells plates. After 72 hours, cells were fixed, stained, and total protein/well was determined. Compound concentration which inhibited growth by 50% (IC_{50}) was determined and is reported below. To test for inhibition of isolated Src, the compounds were tested using the assay procedure described in Lai et al., 1998, with the following assay components, final concentrations, and conditions: 50.0 mM MOPS, 4.02 mM $MgCl_2$, 6.00 mM K_3 citrate (used as a Mg^{2+} buffer to stabilize the free Mg^{2+} at 0.5 mM), 99.0 mM KCl, 10.0 mM 2-mercaptoethanol, 198 μ M ADP, 10 U full length human purified recombinant pp60^{c-src} (Upstate Biotechnology Inc., Lake Placid, New York), 2.00 mM RR-SRC, 4.0% DMSO, pH 7.2, 37 °C. These overall assay conditions have been shown to reproduce the intracellular conditions of pH, temperature, free M^{2+} (0.5 mM), ionic strength, osmolality, ATP/ADP, and reduction potential. The results are in Table VII, below.

TABLE VII**INHIBITION OF THE GROWTH OF HUMAN LUNG CANCER CELL LINE H460 AND THE INHIBITION OF ISOLATED SRC**

Compound	H460 ^a IC_{50} (μ M) ^b	Src IC_{50} (μ M)
1a	35 \pm 0.59	IC_{50} = 40
1z	15 \pm 1.6	NT ^c
1bb	82 \pm 3.5	NT
1dd	33 \pm 0.78	NT

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1yyy	104 ± 10	NT
1cc	30 ± 0.66	NT
1cccc	> 100	NT
1oooo	74 ± 2.7	NT
2f	13 ± 0.46	NT
2s	26 ± 0.34	NT
1bbb	> 100	NT
2g	13 ± 0.56	NT
3q	30 ± 0.34	NT

a H460 – NSCLC cells.

b All compounds were solubilized in DMSO and further diluted in RPMI 1640 containing 5% FCS, 5% NuSerum IV, 2 mM L-glutamine, and 20 mM HEPES.

c NT = not tested.

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These results show that the use of a phenyl group attached to the 3 position of the indole ring can significantly improve the activity of the inhibitor.

10 D. Inhibition of Epidermal Growth Factor Receptor Tyrosine Kinase (EGFR TK), p56 lck, p55 fyn, and PTP-1B

The compounds listed in Table VIII below were tested for inhibition of EGFR TK, a transmembrane receptor tyrosine kinase, p56 lck, a member of the Src family of non-receptor tyrosine kinases, p55 fyn, another member of the Src family of non-receptor tyrosine kinases, and PTP-1B, a phosphotyrosine phosphatase, the opposite of a kinase and a target for type II diabetes and/or obesity. The data in the table are the % inhibition of the indicated enzyme by the compound at a concentration of 10 micromolar. Blanks for a particular enzyme indicate that inhibition was not found.

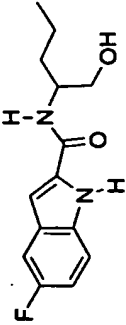
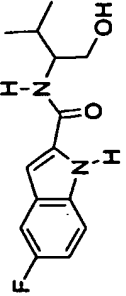
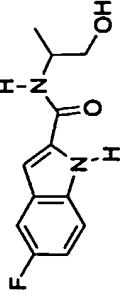
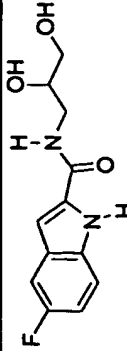
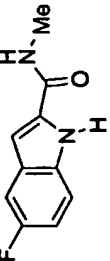
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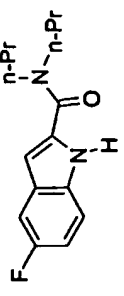
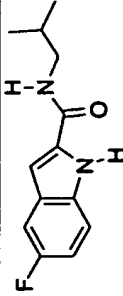
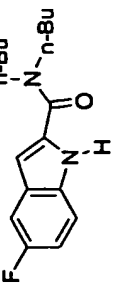
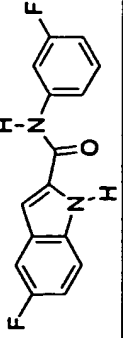
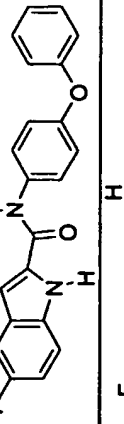
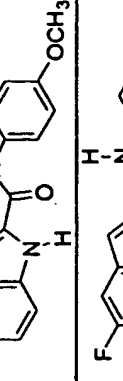
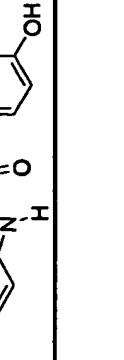
TABLE VIII
INHIBITION OF EGFRPTK, p56 lck, p55 fyn, and PTP-1B

Structure	MW	Compound Code	PTP-1B @ 10 μ m	EGFRTK @ 10 μ m	p56 Lck @ 10 μ m	p55 fyn @ 10 μ m
	264.3	1b				
	264.3	1c				
	236.2	1d				
	252.2	1e				
	192.2	1f				

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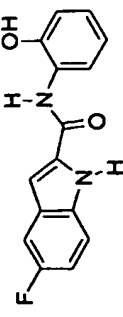
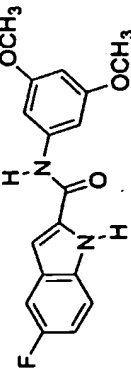
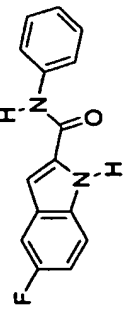
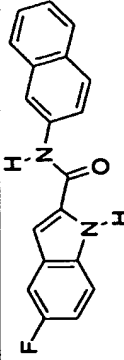
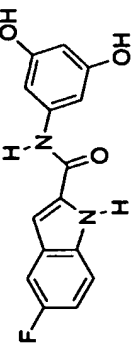
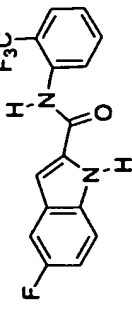
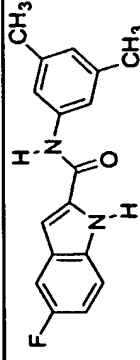
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19					1g	262.3	
					1h	234.3	
					1i	290.4	
					1j	272.3	
13					1k	346.4	
					1l	284.3	
					1m	270.3	

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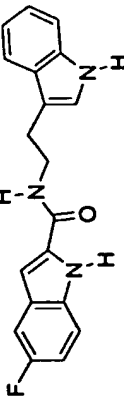
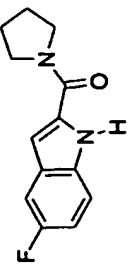
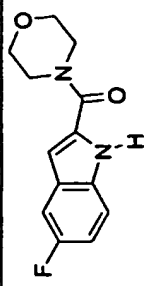
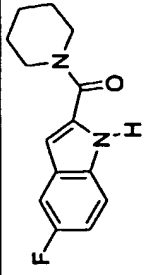
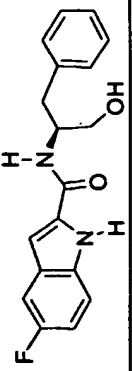
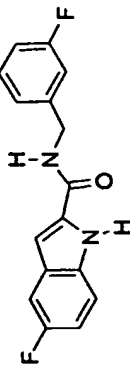
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	270.3	1n				12	
	314.3	1o					
	254.3	1p					
	304.3	1q					
	286.3	1r				11	
	322.3	1s					
	282.3	1t					11

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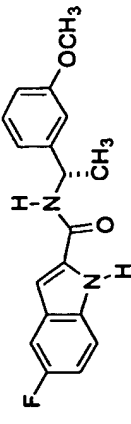
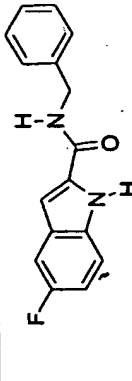
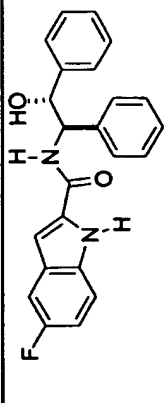
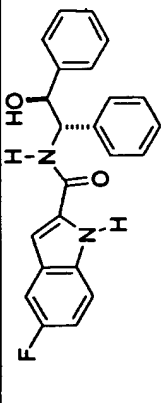
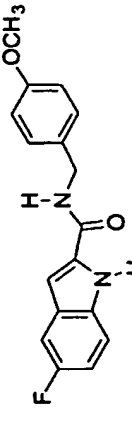
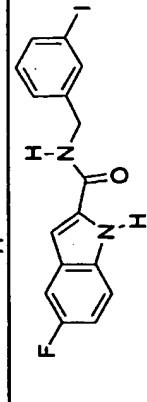
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10					1u	321.4	
					1v	232.3	
10					1w	248.3	
					1x	246.3	
					1y	312.3	
		26			1z	286.3	

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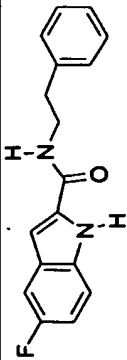
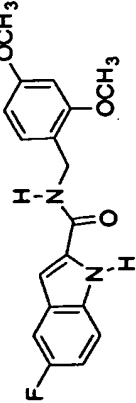
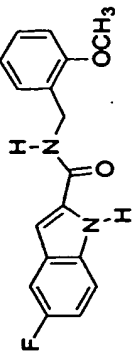
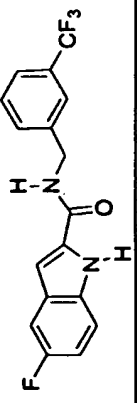
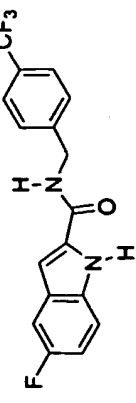
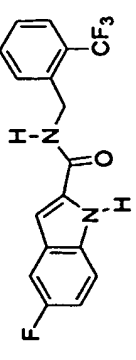
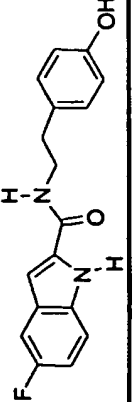
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	312.3	1aa			12		10
	268.3	1bb			19		
	374.4	1cc			19		
	374.4	1dd			41		
	298.3	1ee			16		
	394.2	1ff			24		

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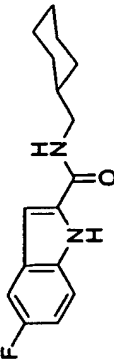
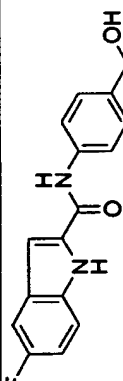
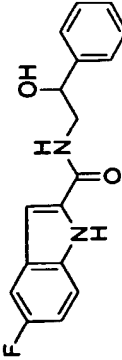
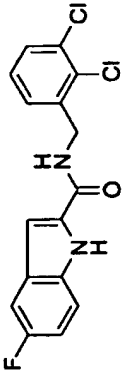
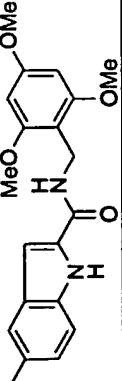
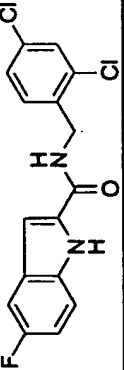
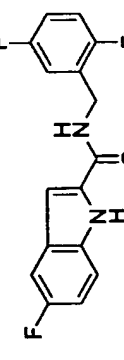
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	282.3	1gg				
	328.3	1hh				
	298.3	1ii				
	336.3	1jj	18			
	336.3	1kk				
	336.3	1ll				
	298.3	1mm				

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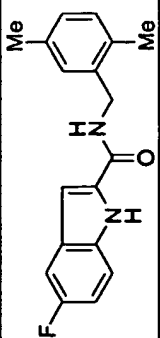
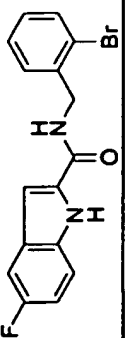
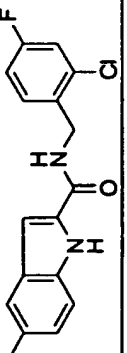
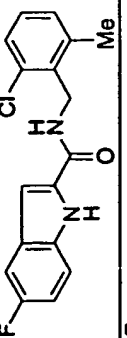
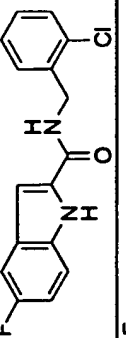
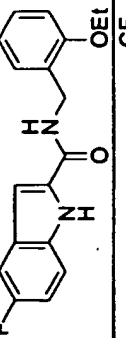
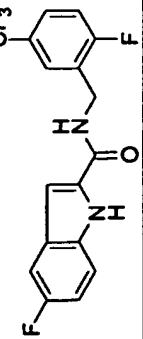
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	274.3	1nn					
	284.3	1oo				17	
	298.3	1pp					
	337.2	1qq					
	358.4	1rr				12	
	337.2	1ss				12	
	304.3	1tt					

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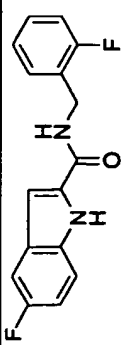
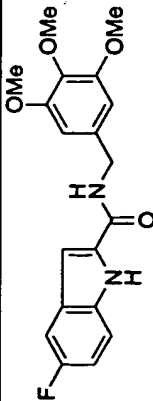
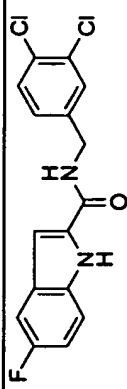
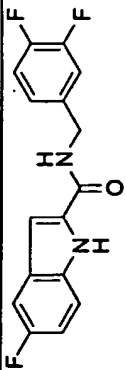
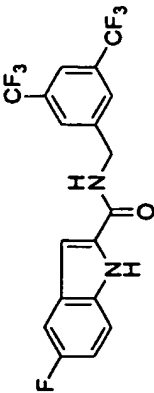
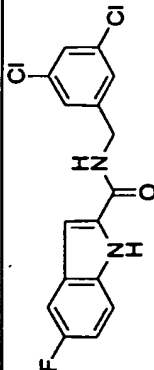
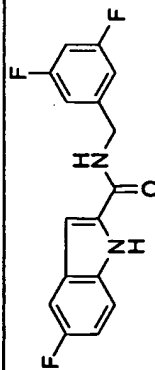
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	296.3	1uu				
	347.2	1vw				
	320.7	1ww				
	316.8	1xx			14	
	302.7	1yy		10	12	
	312.3	1zz				
	354.3	1aaa		12		

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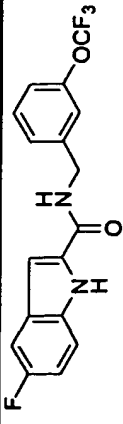
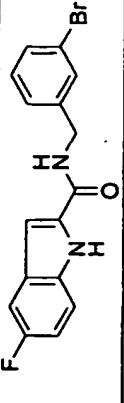
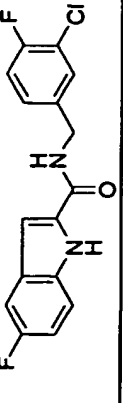
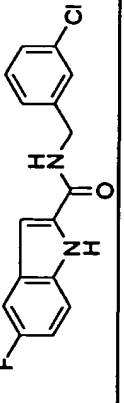
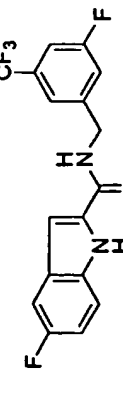
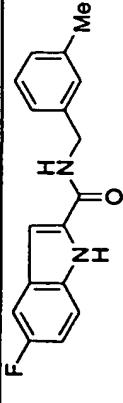
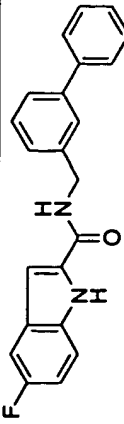
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	286.3	1bbb				
	358.4	1ccc				
	337.2	1ddd				
	304.3	1eee				
	404.3	1fff				
	337.2	1ggg				
	304.3	1hhh				

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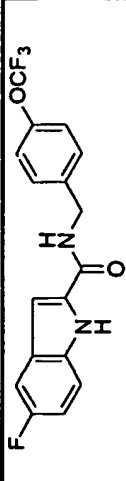
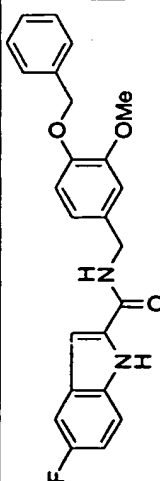
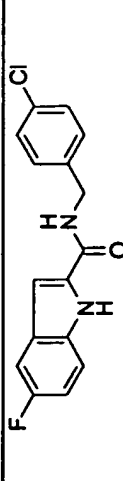
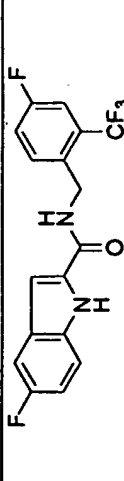
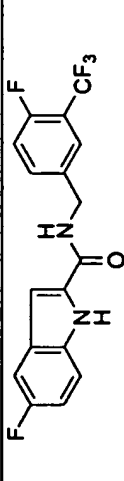
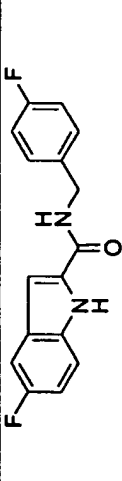
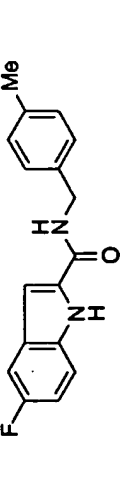
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	352.3	1111				
	347.2	1111				
	320.7	1kkk				
	302.7	1111				
	354.3	1mmn				14
	282.3	1mmn				
	344.4	1ooo				

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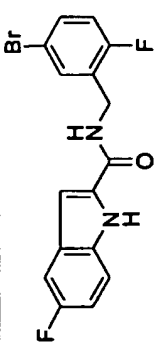
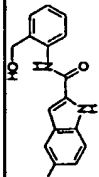
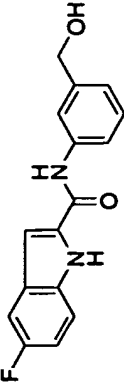
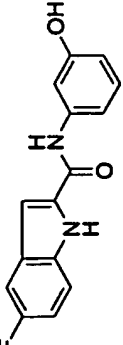
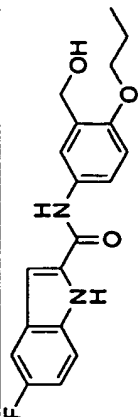
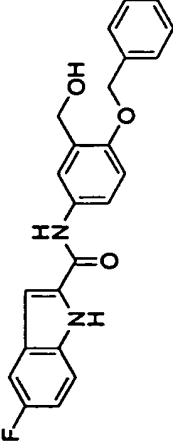
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	352.3	1ppp				
	404.4	1qqq				11
	302.7	1rrr				15
	354.3	1sss				
	354.3	1ttt				
	286.3	1uuu		13		16
	282.3	1vvv				

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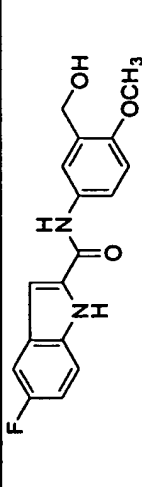
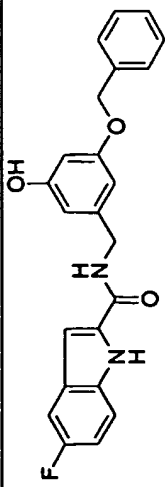
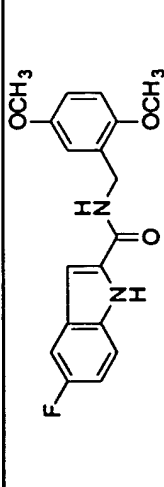
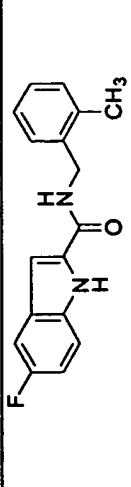
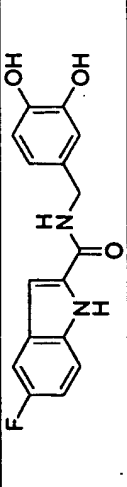
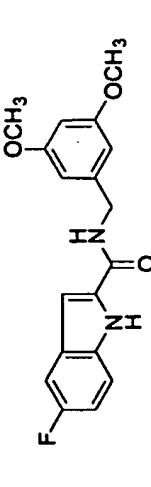
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		11				
	12					
1www	1xxx	1yyy	1zzz	1aaaa	1bbbb	
365.2	284.3	284.3	270.3	342.4	390.4	
						

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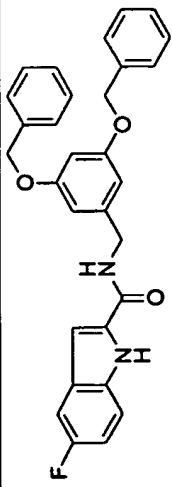
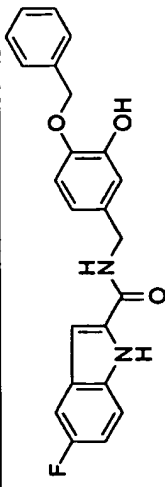
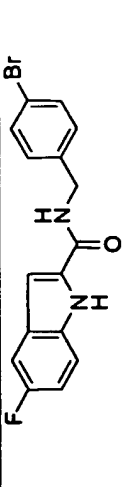
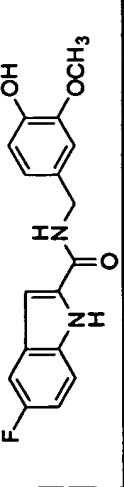
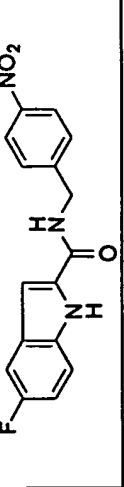
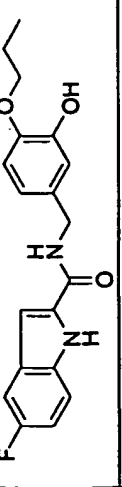
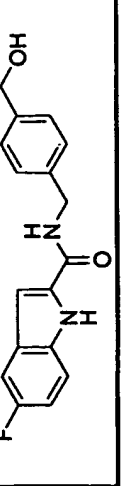
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	390.4	1dddd	16			
	328.3	1eeee				
	282.3	1ffff		12		
	300.3	1gggg		25		
	328.3	1hhhh	17			

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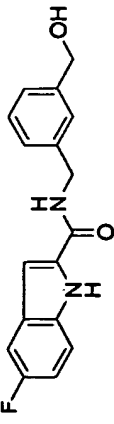
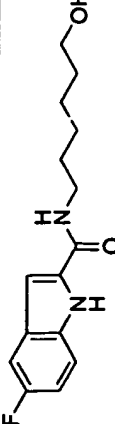
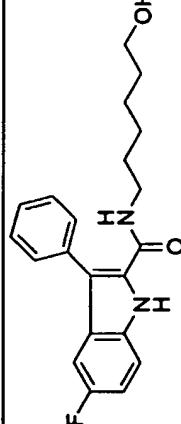
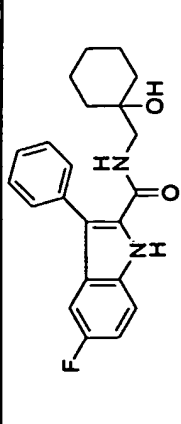
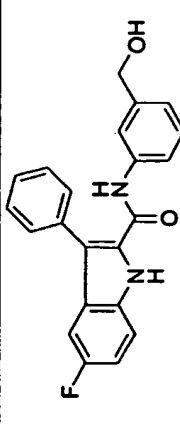
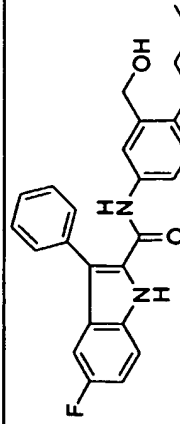
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	480.5	11111			12		
	390.4	11111	15				
	347.2	1kkkk			30		
	314.3	11111					
	313.3	1mmmm				29	
	342.4	1nnnn			17		11
	298.3	1oooo			33		10

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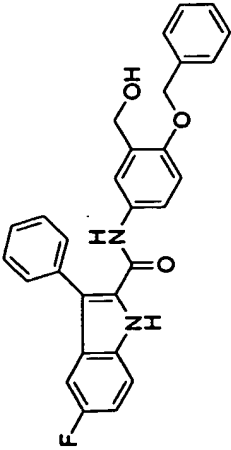
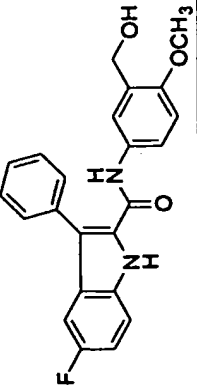
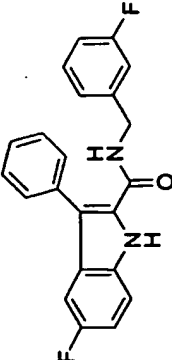
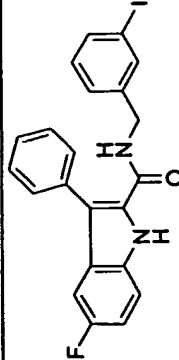
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	298.3	1pppp				
	278.3	1qqqq	18			
	354.4	2a				
	366.4	2b	19			13
	360.4	2c				
	418.5	2d	23			

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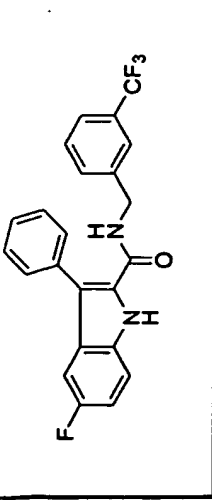
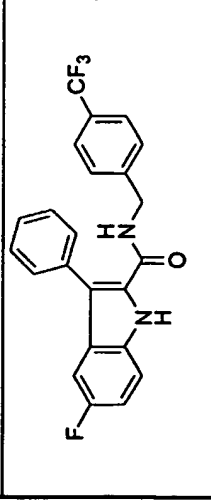
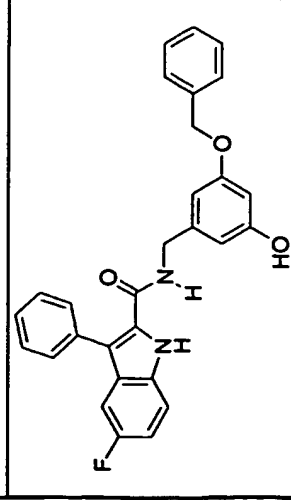
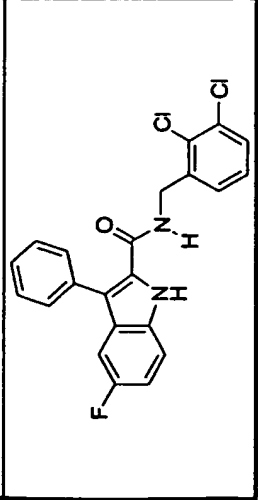
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10		18				
2e	2f	2g	2h			
466.5	390.4	382.4	470.3			
						

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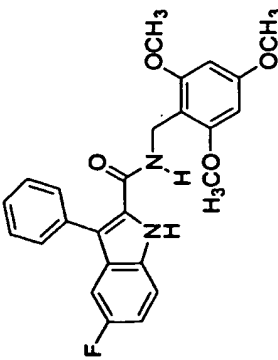
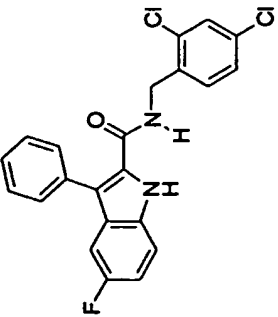
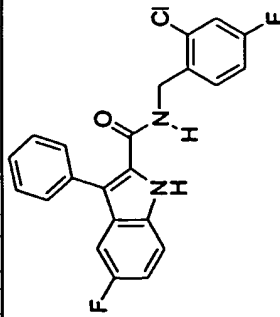
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	20		
2l	2j	2k	2l
412.4	412.4	466.5	413.3
			

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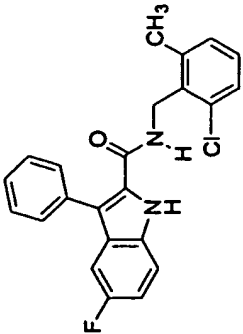
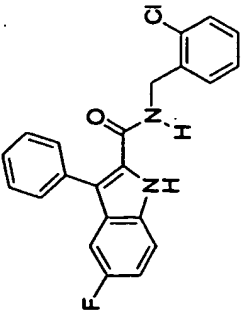
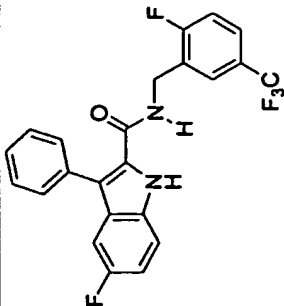
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		12.
2m	2n	2o
434.5	413.3	396.8
		

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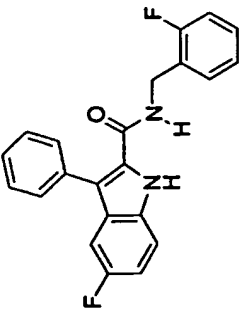
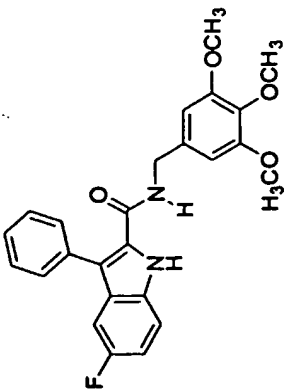
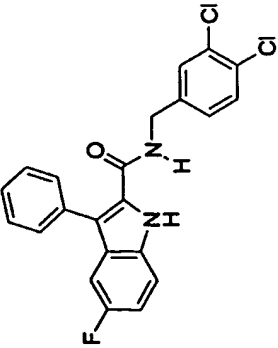
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2p	2q	2r
392.9	378.8	430.4
		

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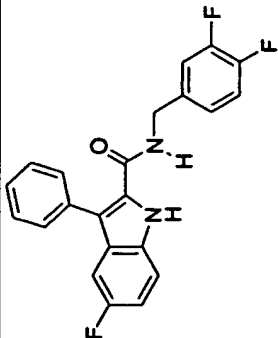
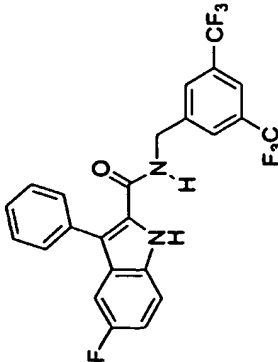
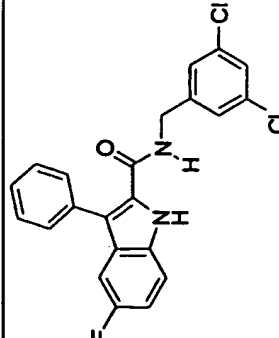
PCT/US02/33660

11		
10		
33		
2e	2t	2u
362.4	434.5	413.3
		

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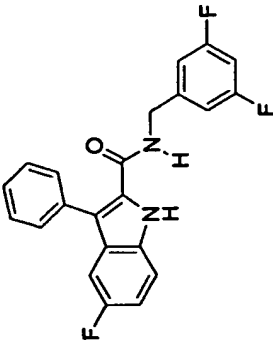
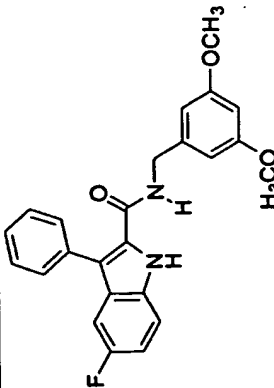
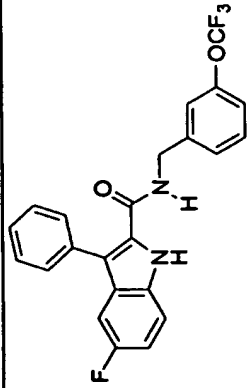
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	12	
2v	2w	2x
380.4	480.4	413.3
		

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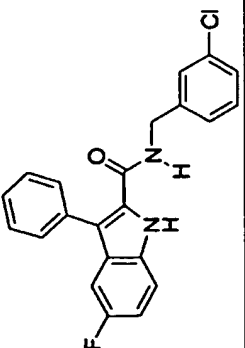
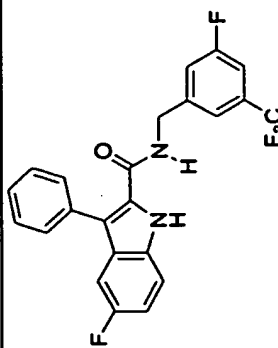
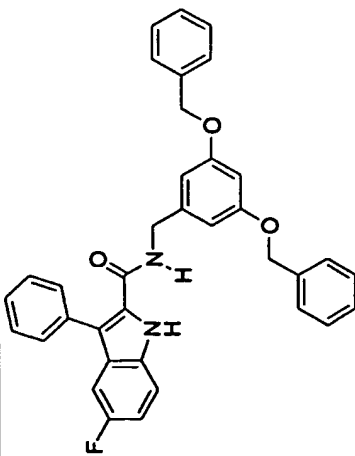
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20		
2y	2z	2aa'
380.4	404.4	428.4
		

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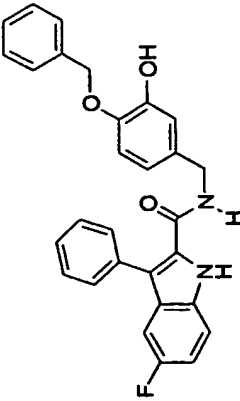
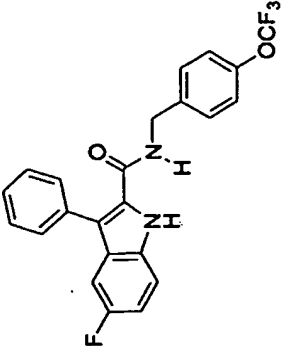
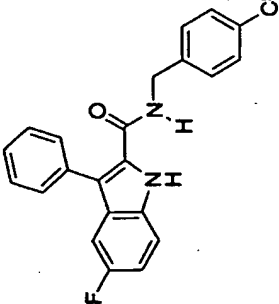
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2bb	2cc	2dd
378.8	430.4	556.6
		

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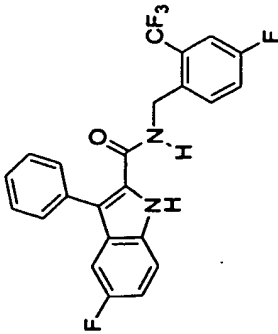
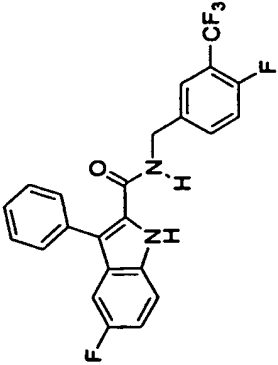
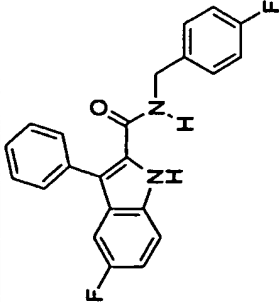
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		12
2ee	2ff	2gg
466.5	428.4	378.8
		

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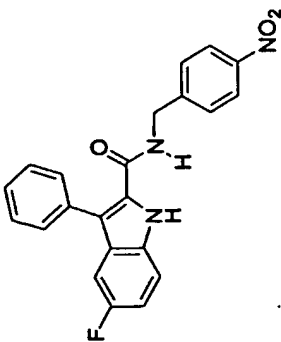
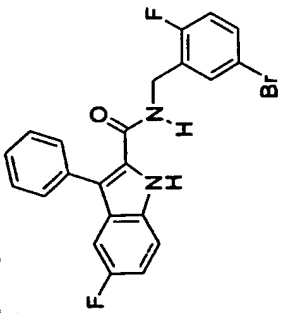
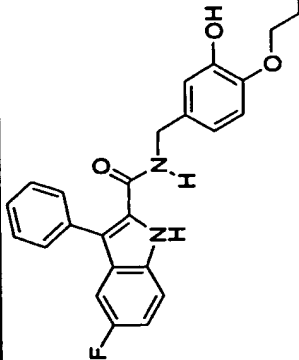
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12		
2hh	2ii	2jj
430.4	430.4	362.4
		

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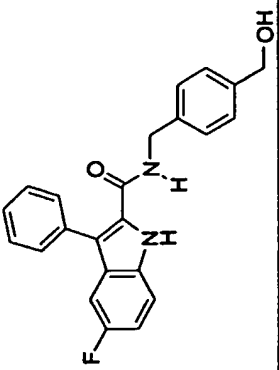
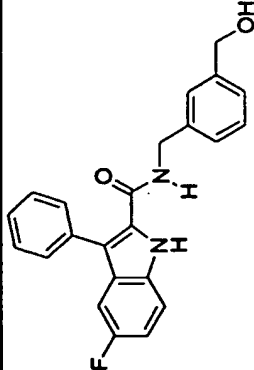
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24			
	10		
2kk	2ll	2mm	
389.4	441.3	418.5	
			

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2 θ	2 θ
374.4	374.4
	

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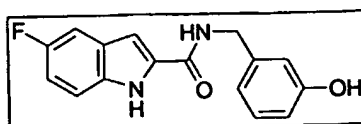
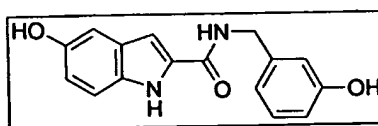
140

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E. Mice Toxicity Study

Figure 15 shows the results of a maximum tolerated dose (MTD) study with two indole inhibitors:

5

**1a****2k from Example 4**

10 These compounds were administered to SCID mice by intraperitoneal administration in tween80:EtOH. The results in Figure 15 show that compound **1a** is less toxic in mice than compound **2k from Example 4**, since the mice exhibited less weight loss when compound **1a** was administered.

15

Example 2 - Synthesis and Activity of 7-Substituted Indole Derivative Protein Kinase Inhibitors

7-substituted indole derivative protein kinase inhibitors were synthesized as
20 set forth in Scheme 1, below:

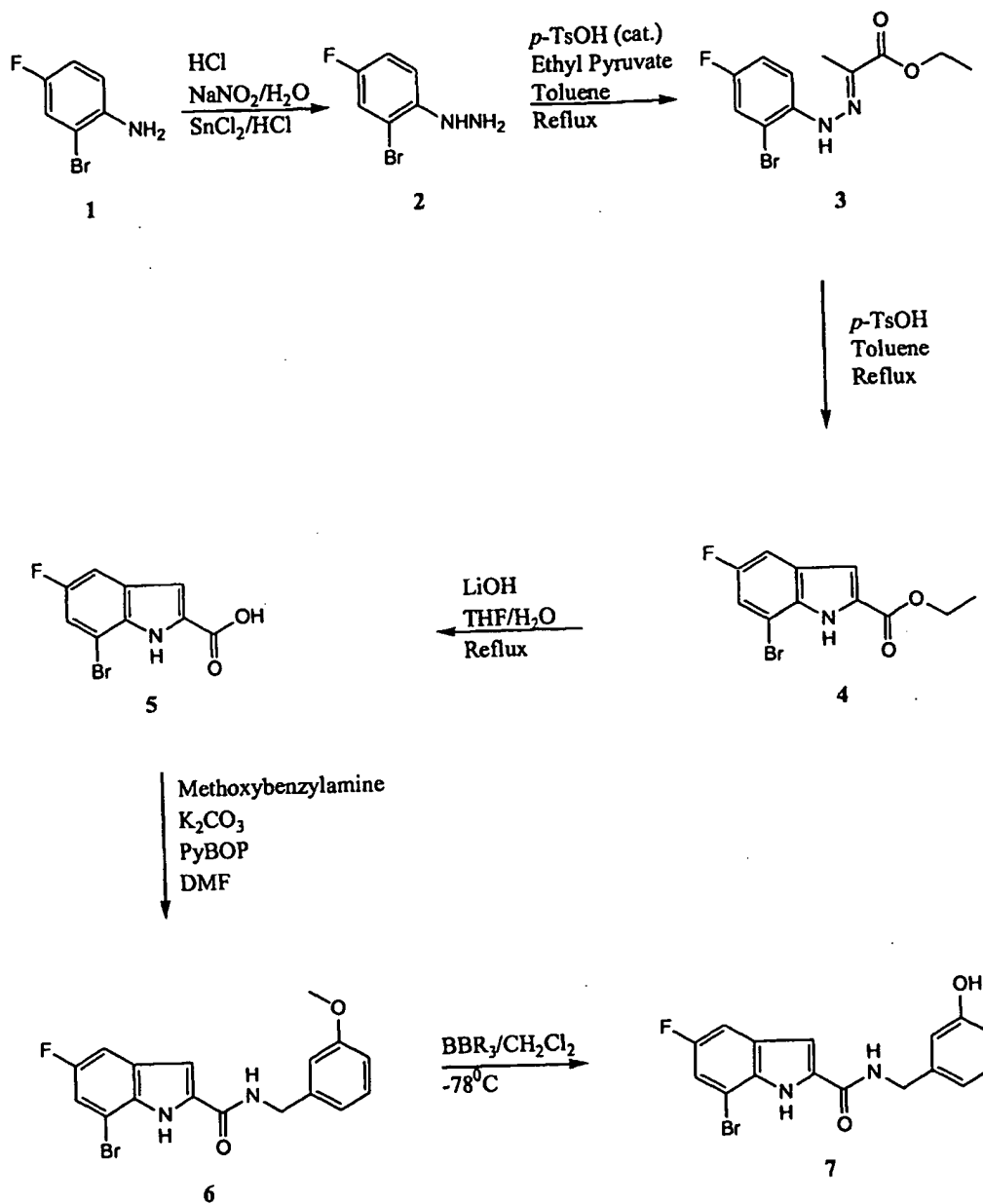
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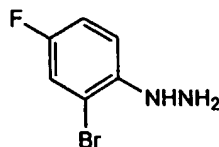
Scheme 1



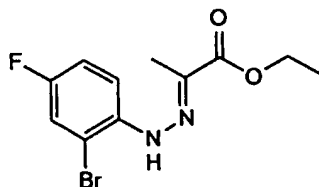
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(2-bromo-4-fluoro-phenyl)-hydrazine (2)

Commercially available 2-bromo-4-fluoroaniline **1** (2.36 ml, 20.75 mmol) was
5 added to a stirring solution of concentrated hydrochloric acid (40 ml) that was cooled
to -5°C . This solution was allowed to age while stirring for 10 minutes. An aqueous
solution of NaNO_2 was added over 15 minutes. SnCl_2/HCl (10.40g, 46.1 mmol, 10 ml
 HCl) was added over 15 minutes and aged for an additional 30 minutes to 1 hour. The
mixture was filtered and washed with dichloromethane. The resulting solid was
10 dissolved in 1.0M HCl and extracted 3 times with dichloromethane. The organic layer
was vacuum dried overnight to give 3.53g (83% yield). ^1H NMR (400 MHz, CDCl_3):
 δ 7.169 (dd, $J=8$ Hz, $J=2.8$ Hz 1H), δ 7.076 (dd, $J=5.2$ Hz, $J=9.2$ Hz, 1H), δ 6.982
(td, $J=8.4$ Hz, $J=2$ Hz 1H), δ 5.540 (bs, 1H), δ 3.590 (bs, 1H).

2-[(2-bromo-4-fluoro-phenyl)-hydrazono]-propionic acid ethyl ester (3)

Commercially available *p*-toluenesulfonic acid (38.37 mg, 0.217 mmol) was
added to 60 ml of toluene in a round bottom flask and magnetic stir bean. The flask
was then fitted with a Dean Stark trap and reflux condenser. The solution was then
20 allowed to stir for 2 hours. After 2 hours, the solution was cooled and 2-(bromo-4-
phenyl)hydrazine (4.135g, 20.17 mmol) was added. The solution was then refluxed
for an additional 1.5 hours using the same apparatus. After 1.5 hours, the solution was
placed on the rotary evaporator to remove the toluene. A dark brown tar-like
substance was left in the flask. An appropriate amount of hexanes were added to the
25 flask and refluxed to dissolve the pure hydrazine. The hexanes took on a yellow color
and were then decanted hot into another flask leaving the tar-like side product behind.

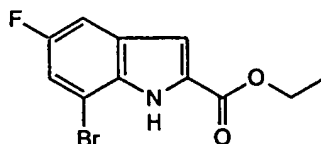
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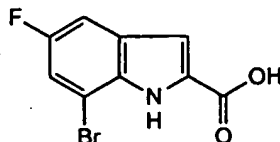
This was repeated. The flask containing the hexane solution was refluxed so as to dissolve the precipitating hydrazine and placed in the freezer to form crystals. 3.6g (11.9 mmol, 87% yield) of 3. ¹H NMR (Acetone-*d*₆): δ 12.369 (bs, 1H), δ 7.646 (dd, *J*=9.2Hz, *J*=5.6Hz 1H), δ 7.449 (dd, *J*=8.2 Hz, *J*=2.8 Hz 1H), δ 7.22 (td, *J*=~8.6 Hz, *J*=2.8 Hz, 1H), δ 4.37 (q, *J*=7.2 Hz, 2H), δ 2.203 (s, 3H), δ 1.402 (t, *J*=7.2 Hz, 3H).

7-bromo-5-fluoro-1H-indole-2-carboxylic acid ethyl ester (4)



Commercially available *p*-toluensulfonic acid dihydrate (2.26g, 11.9 mmol) was added to 120 ml of toluene and dried under reflux using a Dean Stark apparatus for 2 hours. 2-[(2-bromo-4-fluoro-phenyl)-hydrazono]-propionic acid ethyl ester (3.6g, 11.9 mmol), was added to the cooled solution, and refluxed for an additional 1.5 hours. After 1.5 hours the solution was cooled. The toluene was removed under reduced pressure. Then the solid was refluxed with hexane to isolate the indole ester. The resulting hexane solution was refluxed to dissolve the precipitating indole, and placed in the freezer for crystallization. After removal of supernatant and drying of crystals gave 3.30g, 11.543 mmol of 4 (97% yield). ¹H NMR (400MHz, Acetone-*d*₆): δ 10.85 (bs, 1H), δ 7.45 (dd, *J*=9.2 Hz, *J*=2.4 Hz, 1H), δ 7.39 (dd, *J*=9.2 Hz, *J*=2.0 Hz, 1H), δ 7.28 (d, *J*=2.0 Hz, 1H), δ 4.36 (q, *J*=6.8 Hz, 2H), δ 1.345 (t, *J*=6.8 Hz, 3H).

7-bromo-5-fluoro-1H-indole-2-carboxylic acid (5)



Tetrahydrofuran (35.2 ml), water (23.5 ml), lithium hydroxide (2.61g, 10.9 mmol), and 7-bromo-5-fluoro-1H-indole-2-carboxylic acid ethyl ester (3.11g, 10.9

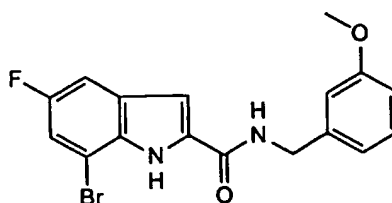
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mmol) were added to a round bottom flask and mixed with a magnetic stirrer. This mixture was refluxed for 1 hour. The THF was removed via rotary evaporator, and the aqueous solution was acidified with 1M HCL, and extracted with ethyl acetate. ¹H NMR (DMSO-*d*₆): δ 13.206 (bs, 1H), δ 11.876 (s, 1H), δ 7.498–7.445 (m, 2H),
5 δ 7.19 (d, *J*=2.0 Hz, 1.0H).

7-bromo-5-fluoro-1H-indole-2-carboxylic acid 3-methoxy-benzylamide (6).



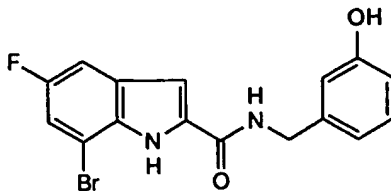
To a round bottom flask that has been fire dried, flushed with a continuous
10 stream of argon, and equipped with a stir bean, DMF (4.8 ml) was added. To this stirring solution 5 (600 mg, 2.33 mmol), was combined with methoxybenzylamine (328μL, 2.56 mmol), and PyBOP (1.33g, 2.56 mmol). This solution was then cooled to a temperature of 0 degrees C. After 2 minutes diisopropylamine (1.7 ml, 9.67 mmol) was added and the entire solution was allowed to stir at room temperature
15 overnight. The reaction was then diluted with roughly 60 ml of ethyl acetate and extracted 3X with saturated sodium bicarbonate, and 3X with 1M HCl in appropriate volumes to remove any unreacted starting materials. The ethyl acetate layer was isolated and dried over sodium sulfate. The ethyl acetate was removed using a rotary evaporator to yield a brownish film on the sides of the flask. Hexanes were added to
20 the flask and refluxed. A solid then formed on the sides of the flask, and the hexanes were removed via rotary evaporator to give 709.0 mg of 6 (81% yield). ¹H NMR (400MHz, DMSO-*d*₆) δ 11.537 (bs, 1H), δ 9.092 (t, *J*=5.6 Hz, 1H), δ 7.49 (dd, *J*=9.4 Hz, *J*=2.4 Hz 1H), δ (dd, *J*=8.8 Hz, *J*=2 Hz 1H), δ 7.268-7.228 (m, 2H), δ 6.91 (d, *J*=6.8 Hz, 2H), δ 6.82 (d, *J*=8.2 Hz, 1H), δ 4.48 (d, *J*=6 Hz, 2H), δ 3.729 (s, 3H).

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7-bromo-5-fluoro-1H-indole-2-carboxylic acid 3-hydroxy-benzylamide (7)

A stirring solution of methylene chloride (1 ml) was cooled to -78 degrees in a dry ice acetone bath and flushed with a stream of argon. To this cold stirring solution
5 6 (50 mg, 0.133 mmol) was added. 7 equivalents of BBr_3 was added and allowed to stir at -78 degrees for 1 hour, and then the solution was allowed to stir at room temperature overnight. The reaction was then quenched with excess water, then neutralized with saturated sodium bicarbonate, and extracted with methylene chloride. The methylene chloride layer was dried over sodium sulfate and removed under
10 reduced pressure to yield 35.0 mg of 2 (70% yield). ^1H NMR (400 MHz, Acetone- d_6) δ 10.633 (bs, 1H), δ 8.42 (d, $J=15.6$, 2H), 7.48 (dd, $J=9.2$ Hz, $J=2.4$ Hz, 1H), δ 7.42 (dd, $J=9$ Hz, $J=2.4$ Hz, 1H), δ 7.373 (d, $J=2.4$ Hz, 1H), δ 7.217 (t, $J=7.6$ Hz, 1H), δ 6.932-6.898 (m, 2H), δ 6.80 (dd, $J=2$ Hz, $J=8$ Hz, 1H), δ 4.634 (d, $J=5.6$ Hz, 2H). Disappearance of the characteristic methoxy peak at 3.7 ppm indicates a successful
15 deprotection.

Example 3 - Design, Synthesis and Activity of Non-ATP Competitive Hydroxynaphthalene Derivative Inhibitors of pp60^{c-Src} Tyrosine Kinase

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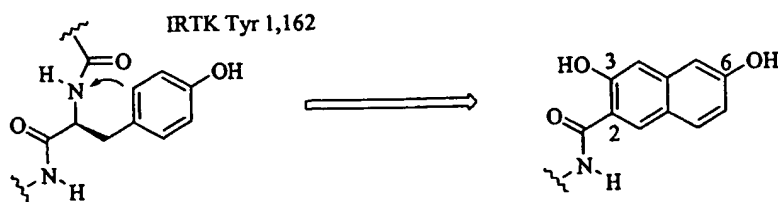
The crystal structure of the autoinhibited human IRTK catalytic domain (Hubbard et al., 1994) was used to carry out qualitative molecular modeling studies (SYBYLTM, 6.4, Tripos Inc., St. Louis) wherein a naphthalene ring was superimposed upon the IRTK Tyr 1,162. The IRTK region containing Tyr 1,162 folds back into the
25 active site, with Tyr 1,162 positioned analogous to a phosphorylatable Tyr in a peptide substrate, thereby autoinhibiting the tyrosine kinase. This superimposition indicated that an amide carbonyl should be placed at the 2-position (Scheme 1) of the

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Scheme 1



naphthalene ring to mimic the Tyr 1,162 carbonyl and a hydroxyl group should be positioned at the 6-position to mimic the Tyr 1,162 hydroxyl group. These modeling studies also indicated that a hydroxyl group at the 3-position could mimic the Tyr

5 1,162 NH.

In order to test these design concepts experimentally, the 2-position carbonyl group was appended as either a methyl ester or as a series of amides (Table IX). The hydroxy N-phenyl (X=0) and N-benzyl (X=1) amides were chosen based upon the increase in pp60^{c-src} inhibitor potency observed with iminochromene analogs

10 containing appended hydroxy N-phenyl amide side-chains (Huang et al., 1995). Analogs wherein the 6-hydroxyl group was either deleted or moved were also prepared to determine if a drop in potency occurs as predicted from the modeling studies.

The series of 2-carbonyl-3,5-dihydroxy naphthalene inhibitors (1a, 2a-2d, 2i-2l, 2o-2p) and 2-carbonyl-3,7-dihydroxy naphthalene inhibitors (1c, 2t-2u) were synthesized from commercially available (Aldrich) 3,5-dihydroxy-2-naphthoic acid and 3,7-dihydroxy-2-naphthoic acid, respectively. The methyl esters 1a and 1c were obtained by refluxing the respective acid starting materials for 48h in methanol pre-saturated with HCl gas. The amides (2a-2d, 2i-2l, 2o-2p, 2t-2u) were synthesized by

20 coupling the respective carboxylic acid with commercially available (Aldrich or Lancaster) amines using one of two methods. The first method utilized the NBS/PPh₃ methodology as described by Froyen (Froyen, 1997). The second method utilized IIDQ (Aldrich) as the coupling reagent. The carboxylic acid was first reacted with 1.0 eq. IIDQ in anhydrous DMF at room temperature for 24 hours. The respective amine

25 (2.0 eq.) was then added neat and the reaction was heated to 80°C for 2-6 hours. After aqueous workup, purification was achieved by silica gel chromatography and precipitation from CH₂Cl₂/hexane, followed by preparative C-18 RP-HPLC (CH₃CN/H₂O), if necessary. The benzyl amines were commercially available only as

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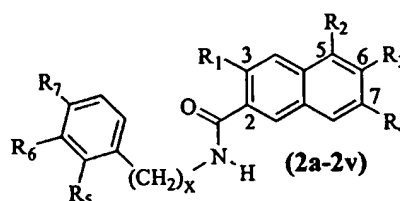
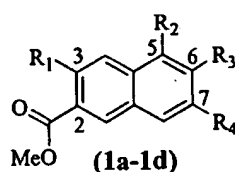
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their corresponding hydroxyl protected methyl ethers. Consequently, after amide formation, the hydroxyl groups were deprotected by treatment with 6 eq. BBr_3 in DCM for 1 minute at -78°C followed by 1 hour at room temperature.

5

TABLE IX

pp60^{c-src} INHIBITORY ACTIVITY OF HYDROXYNAPHTHALENE DERIVATIVES AND SELECT PUBLISHED INHIBITORS.^{a,b,c}



Cmpd	R ₁	R ₂	R ₃	R ₄	R ₅	R ₆	R ₇	R ₈	% Inhibition at 100 μM (std. dev.)	IC ₅₀ (μM)
1a	OH	OH	H	H	N/A	N/A	N/A	N/A	5 (+/-2)	n.t.
1b	OH	H	OH	H	N/A	N/A	N/A	N/A	47 (+/-3)	n.t.
1c	OH	H	H	OH	N/A	N/A	N/A	N/A	19 (+/-6)	n.t.
1d	NH ₂	H	H	H	N/A	N/A	N/A	N/A	Inactive	n.t.
2a	OH	OH	H	H	OH	H	H	0	12 (+/-4)	n.t.
2b	OH	OH	H	H	H	OH	H	0	51 (+/-1)	150
2c	OH	OH	H	H	H	H	OH	0	60 (+/-7)	n.t.
2d	OH	OH	H	H	OH	H	OH	0	14 (+/-2)	n.t.
2e	OH	H	OH	H	OH	H	H	0	39 (+/-5)	n.t.
2f	OH	H	OH	H	H	OH	H	0	89 (+/-1)	16
2g	OH	H	OH	H	H	H	OH	0	23 (+/-5)	n.t.
2h	OH	H	OH	H	OH	H	OH	0	56 (+/-1)	n.t.
2i	OH	OH	H	H	H	OMe	H	0	33 (+/-5)	n.t.
2j	OH	OH	H	H	H	H	OMe	0	35 (+/-8)	n.t.
2k	OH	OH	H	H	OMe	H	H	1	13 (+/-3)	n.t.
2l	OH	OH	H	H	H	H	OMe	1	14 (+/-2)	n.t.
2m	OH	H	OH	H	OMe	H	H	1	inactive	n.t.
2n	OH	H	OH	H	H	H	OMe	1	4 (+/-7)	n.t.
2o	OH	OH	H	H	OH	H	H	1	41 (+/-2)	n.t.
2p	OH	OH	H	H	H	H	OH	1	49 (+/-4)	n.t.
2q	OH	H	OH	H	OH	H	H	1	42 (+/-2)	n.t.
2r	OH	H	OH	H	H	OH	H	1	55 (+/-3)	n.t.
2s	OH	H	OH	H	H	H	OH	1	42 (+/-3)	n.t.
2t	OH	H	H	OH	H	OH	H	0	68 (+/-5)	n.t.
2u	OH	H	H	OH	H	OH	H	1	40 (+/-3)	n.t.
2v	H	H	OH	H	H	OH	H	0	45 (+/-5)	n.t.

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Iminochromene 9TA	30 (+/-15)	Lit ⁸ : 0.118
Piceatannol	41 (+/-2)	Lit ¹³ : 66 (Ick)
ST-638	37 (+/-5)	Lit ¹⁴ : 18
Emodin ^d	22 (+/-3)	Lit ¹⁵ : 38
Tyrophostin A47	43 (+/-3)	

Table IX Footnotes:

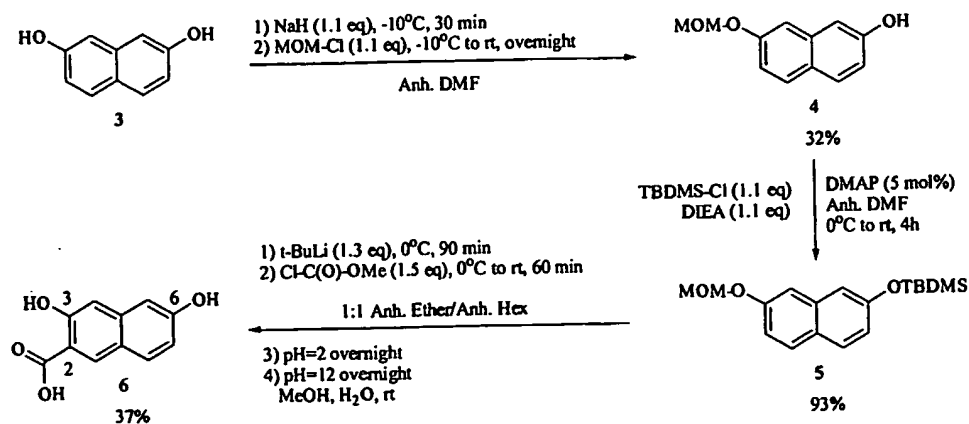
^a The previously described assay procedure (Lai et al., 1998) was used with the following assay components, final concentrations and conditions: 50.0 mM MOPS, 4.02 mM MgCl₂, 6.00 mM K₃citrate (used as a Mg²⁺ buffer to stabilize the free Mg²⁺ at 0.5 mM), 99.0 mM KCl, 10.0 mM 2-mercaptoethanol, 198 μM ATP, 19.8 μM ADP, 10 U full length human purified recombinant pp60^{c-src} (Upstate Biotechnology Inc.), 2.00 mM RR-SRC, 4.0 % DMSO, pH 7.2, 37°C. These overall assay conditions have been shown (Choi, 1999) to reproduce the intracellular conditions of pH, temp., free Mg²⁺ (0.5 mM), ionic strength, osmolality, ATP/ADP and reduction potential.

^b All new compounds were characterized by proton NMR, EI or FAB(+) MS and are pure by TLC.

^c N/A = Not applicable, n.t. = Not tested.

^d ATP-competitive.

The series of 2-carbonyl, 3,6-dihydroxy naphthalene inhibitors (1b, 2e-2h, 2m-2n, 2q-2s) were synthesized from 3,6-dihydroxy-2-naphthoic acid 6 using the methods described above. The synthesis of intermediate 6 that was developed is shown in Scheme 2 beginning with commercially available 2,7-dihydroxynaphthalene 3 (Aldrich).



Compound 1d was synthesized from 3-amino-2-naphthoic acid (Aldrich) by reaction with TMS-diazomethane in DCM at room temperature. Compound 2v was

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synthesized from 6-hydroxy-2-naphthoic acid (Aldrich) using the amidation method described by Froyen (Froyen, 1997).

Kinase assay conditions have been shown to influence the measured inhibitory activity (Lawrence et al., 1998). Consequently, in order to accurately determine the relative potency of the newly designed class of pp60^{c-src} inhibitors, the inhibitory activity of four previously published, non-ATP competitive PTK inhibitors, was also tested. Piceatannol, ST-638, and Tyrphostin A47 were chosen because they are commercially available (Sigma or Calbiochem), and are representative of the spectrum of known non-ATP competitive PTK inhibitors. Emodin (Calbiochem) is ATP-competitive when analyzed with the tyrosine kinase p56^{lck}. Previously, iminochromene 9TA was the most potent non-ATP competitive pp60^{c-src} inhibitor reported (Huang et al., 1995). Since iminochromene 9TA was not commercially available, it was synthesized using a novel route by converting 3-Aminophenol to the corresponding TBDMS ether (1.1 eq. TBDMS-Cl, 1.1 eq. DIEA, 5 mol% DMAP, DMF, 24 h, rt, 71%). The resulting aniline was coupled using 2.0 eq. of cyanoacetic acid (1.1 eq. EDCI, 1.1 eq. TEA, DMF, 18 h, 75°C, 70%). Condensation of the resulting amide with 1.2 eq. of 2,3-dihydroxybenzaldehyde (cat. piperidine, abs. EtOH, 2 h, 60°C) followed by deprotection (1.1 eq. TBAF, THF, 15 m, 43% overall) gave iminochromene 9TA with satisfactory elemental, FAB(+)MS and ¹H NMR analysis after purification by flash chromatography (10:1, DCM:MeOH).

The inhibitory activities shown in Table IX for compounds 1a-d and 2a-2v were determined using purified, full length, human recombinant pp60^{c-src}. Due to the number of compounds tested, and the associated cost, their rank order potencies were first determined at a constant inhibitor concentration (100 μM). As predicted by the modeling studies, based upon analogy to the IRTK Tyr 1,162 hydroxyl group, a preference for positioning the naphthalene hydroxyl group on carbon 6 vs. 5 or 7 was observed in both the ester (1b, 47% vs. 1a, 5% & 1c, 19%) and amide (e.g. 2f, 89% vs. 2b, 51% & 2t, 68%) series. The prediction that attaching a hydroxyl group at naphthalene carbon 3 (mimicking the Tyr 1,162 NH) would improve potency was also confirmed (2f, 89% vs. 2v, 45%). Finally, the prediction that extending the inhibitor

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as an amide at the 2 position (mimicking the peptide bond) could further improve potency was confirmed as well (e.g. **2f**, 89% vs. **1b**, 47%).

The data provided in Table IX demonstrate that moving the hydroxyl group from the optimal 6 position to the adjacent naphthalene carbon 5 results in a different structure activity profile with regard to the optimal concurrent positioning of the hydroxyl group(s) in the amide side chain (e.g. **2f/2g** vs. **2b/2c**). Also of note is the replacement of the amide side chain hydroxyl group with a corresponding methoxy group in compounds **2i-2n**. In the case of the N-phenyl amides (**2i-2j**), their activity, relative to the corresponding hydroxy amides (**2b-2c**), was not reduced as significantly as in the case of the N-benzyl amides (**2k-2n** vs. **2o-2q**, **2s**). This suggests that in the benzyl derivatives, the amide side chain hydroxyl groups either interact with the enzyme as hydrogen bond donors, or the methoxy groups are too large to fit in the binding site.

A more quantitative analysis of the selectivity for positioning a hydroxyl group on carbon 6 vs. 5 is provided by comparing the IC_{50} 's of **2f** (16 μ M) vs. **2b** (150 μ M), respectively. These results also confirm that a drop in % inhibition from ca. 90% to ca. 50% represents an order of magnitude difference in potency, as expected. Similarly, a drop in % inhibition from ca. 50% to 10% would represent another order of magnitude difference in potency.

A direct comparison of the most potent inhibitor from this series, compound **2f**, with the five previously reported PTK inhibitors shown in Table IX demonstrates that, under these assay conditions, **2f** is more potent by one to two orders of magnitude. Interestingly, iminochromene 9TA was previously reported (Huang et al., 1995) to have an IC_{50} of 118 nM against pp60^{c-src}, and was the most potent known non-ATP competitive pp60^{c-src} inhibitor, but under the current assay conditions only a 30% inhibition at 100 μ M was observed. These results re-emphasize (Lawrence et al., 1998) the importance of comparing protein kinase inhibitors under identical assay conditions.

A goal of these studies was to obtain non-peptide pp60^{c-src} inhibitors which do not compete with ATP. Consequently the % inhibition of pp60^{c-src} by **2f** and **2b** at constant inhibitor concentrations was monitored as a function of increasing [ATP] up

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to a cellular mimetic 1 mM level. Since the [ATP] had little effect on the % inhibition, both **2f** and **2b** are non-competitive inhibitors with respect to ATP. The % inhibition was measured using ATP concentrations of 200, 500 & 1,000 μ M while holding the inhibitor concentration constant. If the inhibitor is directly competing with ATP, then this 5-fold overall increase in [ATP] is equivalent to decreasing the inhibitor concentration 5-fold in terms of the effect on % inhibition. Consequently the % inhibition should decrease to the value observed in the IC₅₀ dose-response curve (obtained with 200 μ M ATP) for 1/5 of the set inhibitor concentration used in this experiment if direct competition with ATP is occurring. For inhibitor **2f** (set at 25 μ M) a 62% (+/-5), 54% (+/-3) and 50% (+/-1) inhibition at 200 μ M, 500 μ M and 1,000 μ M ATP, respectively, was obtained whereas the level of inhibition should have dropped to ca. 20% at 1,000 μ M ATP if direct competition with ATP were occurring. Similarly, for inhibitor **2b** (set at 300 μ M) an 84% (+/-1), 81% (+/-1) and 77% (+/-2) inhibition at 200 μ M, 500 μ M and 1,000 μ M ATP, respectively, was obtained. The high cost of many kinases has stimulated other researchers to monitor inhibitor potency as a function of increasing [ATP] for the same purpose (Saperstein et al., 1989; Burke et al., 1993; Davis et al., 1989; Davis et al., 1992; Faltynek et al., 1995; and Sawutz et al., 1996).

In summary, structure-based design has produced a series of hydroxynaphthalene pp60^{c-src} non-peptide inhibitors that do not compete with ATP. Results with compounds from this series in cell-based assays, as well as detailed kinetic studies under various assay conditions, will be reported in due course. An extension of these design concepts from the naphthalene scaffold to an indole scaffold is reported in the following Example.

Example 4 - Design, Synthesis and Activity of Non-ATP Competitive Hydroxyindole Derivative Inhibitors of pp60^{c-src} Tyrosine Kinase

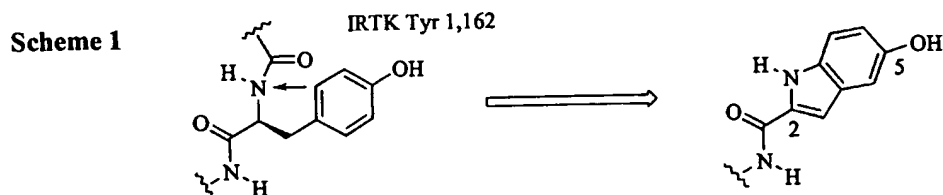
In the preceding example, the structure-based design of a series of pp60^{c-src} inhibitors utilizing a naphthalene scaffold is described. These compounds were designed to bind in the peptide substrate site because of the potential for greater

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selectivity and efficacy in a cellular environment relative to the alternative ATP substrate site. This example presents an extension of these design concepts to a series of pp60^{c-src} inhibitors based upon an indole scaffold. Once again the crystal structure of the autoinhibited insulin receptor PTK (IRTK) was used to carry out qualitative molecular modeling studies, except in this case an indole ring was superimposed upon the IRTK Tyr 1,162. This superimposition indicated that the indole NH can mimic the Tyr 1,162 NH, that a carbonyl should be placed at the 2-position, and a hydroxyl group at the 5 position to mimic the Tyr 1,162 carbonyl and OH, respectively (Scheme 1).



10

The conceptual cyclization of Tyr 1,162 to the smaller 5-membered ring of an indole illustrated in Scheme 1, relative to a 6-membered ring in the case of the naphthalene scaffold (Karni et al., 1999), results in a movement of the optimal positioning of the OH from carbon 6 in the naphthalene scaffold to carbon 5 in the indole scaffold.

15 The indole amide derivatives containing hydroxy phenyl/benzyl side chains **2d-f**, **2j-l** (Table X), respectively, were selected based upon the increase in pp60^{c-src} inhibitor potency observed for the analogous naphthalene-based hydroxy phenyl amides reported in the previous example. The corresponding methyl ethers **2a-c,g-i,v** are precursors in the synthesis. The additional analogs shown in Table X were prepared to begin expanding the range of side chains beyond the hydroxy/methoxy groups that have now been extensively probed with both the indole and naphthalene scaffolds.

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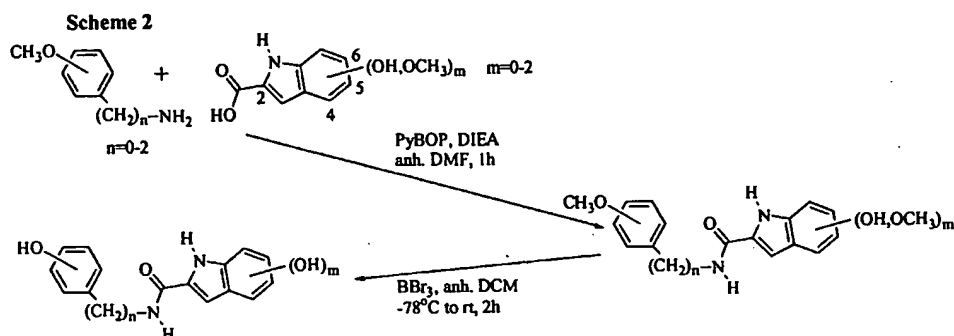
The indole amides containing only hydroxy or methoxy side chains were synthesized as illustrated:

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The 2-indolecarboxylic acid derivative, the methoxyphenyl amine (1.1 eq, Aldrich, Lancaster or Fluka), and the coupling reagent PyBOP (benzotriazol-1-yloxy)tripyrrolidino-phosphonium-hexafluorophosphate) (1 eq, Fluka) were dissolved in anhydrous DMF. The solution was cooled to 0°C under argon and then

10 diisopropylethylamine (DIEA, 3 eq) was added. The reaction was stirred at 0°C for 1m followed by 1 hour at room temperature. After workup the residue was purified by silica gel chromatography.

The methyl ethers were cleaved with boron tribromide (1 M in DCM, Aldrich) when desired. The indole amide methyl ether was suspended in dry DCM and cooled

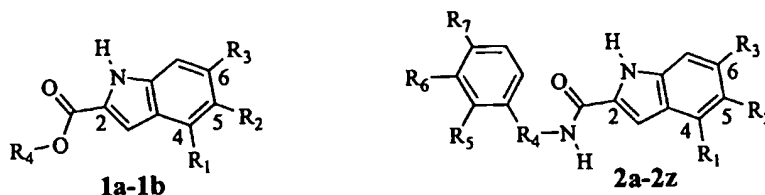
15 to -78°C under argon. One equivalent of BBr_3 was added for each heteroatom in the starting material plus one excess equivalent. The resulting dark red solution was stirred at -78° for 30m and then at room temperature for 1-2 hours. The reaction was quenched with water (10 minutes) before workup.

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TABLE X
pp60^{c-src} INHIBITORY ACTIVITY OF HYDROXYINDOLE
DERIVATIVES.^{a,b,c}



Cmpd	R ₁	R ₂	R ₃	R ₄	R ₅	R ₆	R ₇	% Inhibition at 100 μM (std. dev.)
1a	H	OH	H	CH ₃	N/A	N/A	N/A	40 (+/-5) [at 500 μM]
1b	H	OH	OH	CH ₂ CH ₂	N/A	N/A	N/A	28 (+/-3)
2a	H	OH	H	--	OCH ₃	H	H	3 (+/-1)
2b	H	OH	H	--	H	OCH ₃	H	21 (+/-2)
2c	H	OH	H	--	H	H	OCH ₃	39 (+/-9)
2d	H	OH	H	--	OH	H	H	43 (+/-1)
2e	H	OH	H	--	H	OH	H	30 (+/-6)
2f	H	OH	H	--	H	H	OH	45 (+/-3)
2g	H	OH	H	CH ₂	OCH ₃	H	H	21 (+/-5)
2h	H	OH	H	CH ₂	H	OCH ₃	H	7 (+/-6)
2i	H	OH	H	CH ₂	H	H	OCH ₃	18 (+/-4)
2j	H	OH	H	CH ₂	OH	H	H	24 (+/-3)
2k	H	OH	H	CH ₂	H	OH	H	74 (+/-2)
								[IC ₅₀ = 38 μM]
2l	H	OH	H	CH ₂	H	H	OH	54 (+/-2)
2m	H	OH	H	CH ₂ CH ₂	H	H	OH	21 (+/-7)
2n	H	OH	H	CH ₂	H	H	CO ₂ H	not active
2o	H	OH	H	CH ₂	H	H	CO ₂ CH ₃	11 (+/-4)
2p	H	OH	H	--	H	H	CH ₂ CO ₂ H	7 (+/-6)
2q	H	OH	H	--	H	H	CH ₂ CO ₂ CH ₃	32 (+/-7)
2r	H	OH	H	--	H	F	H	21 (+/-7)
2s	H	OH	H	CH ₂	H	F	H	57 (+/-6)
2t	H	OH	OH	CH ₂	H	OH	H	26 (+/-2)
2u	H	H	OH	CH ₂	H	OH	H	56 (+/-6)
2v	H	H	H	CH ₂	H	H	OCH ₃	4 (+/-4)
2w	H	H	H	CH ₂	H	H	OH	36 (+/-4)
2x	OH	H	H	CH ₃	H	OH	H	60 (+/-3)
2y	H	OH	H	CH(CH ₃) R	H	OH	H	15 (+/-3)
2z	H	OH	H	CH(CH ₃) S	H	OH	H	13 (+/-7)

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^a All compounds were tested as described in the preceding Example.⁵

^b All compounds were characterized by proton NMR, FAB(+) MS and are pure by TLC.

5 ^c N/A = Not applicable.

Using this synthetic route, the series of 5-hydroxyindole amide inhibitors 2a-m,y,z were prepared from 5-hydroxy-2-indolecarboxylic acid. The 4- and 6-hydroxyindole amides (2x,u, respectively) were synthesized from methyl 4-methoxy-2-indolecarboxylate and methyl 6-methoxy-2-indolecarboxylate, respectively. The 10 5,6-dihydroxyindole amide 2t was prepared from ethyl 5,6-dimethoxyindole-2-carboxylate. Sonication of the esters in 1 N NaOH for 1 hour provided the corresponding carboxylic acids for coupling. The des-hydroxy indole amides 2v,w were synthesized from indole-2-carboxylic acid. All of the indole starting materials 15 were commercially available (Aldrich or Lancaster).

The fluoro inhibitors 2r,s were likewise prepared from the corresponding fluorophenyl amines (Aldrich). The inhibitors containing esters or carboxylic acids on the amide side chain, 2n-q, were prepared from the corresponding amino carboxylic acids (Aldrich). The side chain carboxylic acid was first protected as a 20 methyl ester (anh. MeOH pre-saturated with HCl, reflux, 1d), followed by PyBOP coupling (as above), then saponification back to the carboxylic acid when desired.

The methyl ester 1a was prepared by refluxing a solution of the carboxylic acid overnight in anhydrous methanol pre-saturated with HCl gas. The ethyl ester 1b was prepared by BBr₃ deprotection of ethyl 5,6-dimethoxyindole-2-carboxylate as 25 above. All of the inhibitors listed in Table X were purified by silica gel chromatography.

As in Marsilje 2000, the rank order activity of this series of pp60^{c-src} inhibitors was first determined at a constant inhibitor concentration (Table X). The same inhibitor concentration (100 μM) was used for the current indole series of inhibitors, 30 the previous naphthalene series of inhibitors, and five non-ATP competitive literature PTK inhibitors (see preceding example). This allowed an efficient rank order comparison of 59 compounds in total under identical assay conditions.

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The modeling studies predicted that a hydroxy group at carbon 5 of the indole scaffold would be optimal. Comparison of the 5-hydroxy indole inhibitor **2k** (74%) with the analogous 6-hydroxy indole inhibitor **2u** (56%) and 4-hydroxy indole inhibitor **2x** (60%) confirms this prediction, although the preference is not strong.

- 5 The prediction that a hydroxy group at carbon 5 will improve the activity (relative to no hydroxy group) is confirmed by comparing the 5-hydroxy indole inhibitor **2l** (54%) with the corresponding des-hydroxy inhibitor **2w** (36%).

Extending the indole inhibitors as aryl amides at carbon 2 improved potency, as expected based upon the previous naphthalene inhibitors. For example, the meta-hydroxybenzyl amide indole **2k** gives 74% inhibition at 100 μ M whereas the
10 analogous methyl ester **1a** gives only 40% inhibition at 500 μ M. Interestingly, comparing the 5,6-dihydroxy ethyl ester **1b** (28%) to the corresponding aryl amide **2t** (26%) shows that the simultaneous presence of the second hydroxy at carbon 6 prevents the potency enhancement normally provided by the otherwise preferred
15 meta-hydroxybenzyl amide side chain. This amide side chain was the best of the current series when the 5-hydroxyl group is present alone (**2k**, 74%) and still gave good inhibition when a 6-hydroxy group was present alone (**2u**, 56%). Also, the simultaneous presence of two hydroxy groups at carbons 5 and 6 seems well tolerated in the absence of an amide side chain (**1b** vs. **1a** and **2e**). This data suggests that a
20 change in the binding orientation of the indole scaffold may have occurred due to the presence of the second hydroxy group and that a different amide side chain may now be preferred. The optimal combination of side chains at carbons 4-7 (including functional group replacements for hydroxy groups (Lai et al., 1999)) and amide side chains is currently under investigation.

- 25 In general, the indole scaffold structure-activity-relationships ("SARs") revealed by the data in Table X parallels that reported in the preceding example for the naphthalene scaffold. In both cases positioning a hydroxy group on the scaffold analogous to the Tyr 1,162 OH, as identified by modeling studies, provided the highest potency. Moving this hydroxy group to one of the adjacent carbons reduced
30 the potency, but not dramatically, in both cases. Extending both scaffolds with aryl amides at the position identified by the modeling studies to mimic the Tyr 1,162 peptide bond improved the potency. With both scaffolds, substitution of a methoxy

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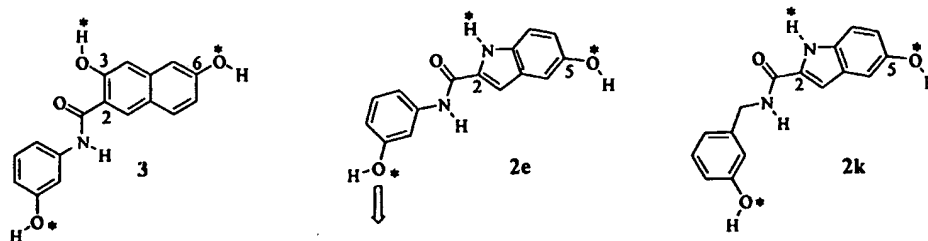
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group for the hydroxy groups on the amide side chain usually reduced potency, and did so to a greater extent with the longer benzylamide side chain (e.g. **2k**, 74% vs. **2h**, 7% compared to **2e**, 30% vs. **2b**, 21%). The major difference in the SARs for these two scaffolds is that the 5-hydroxyindole scaffold prefers the longer m-hydroxybenzyl amide side chain (**2k**, 74% vs. **2e**, 30%) whereas the analogous 3,6-dihydroxynaphthalene scaffold prefers the shorter amide side chain derived from m-hydroxyaniline. The 5-hydroxyindole scaffold showed essentially no preference for the position of the hydroxyl group on the shorter amide side chain (**2d-f**) whereas with the longer hydroxybenzyl amide side chain a significant preference for the meta position was observed (**2j-l**). In the case of the 3,6-dihydroxynaphthalene scaffold the opposite was observed.

Additional molecular modeling studies were carried out to further probe the preference for a longer amide side chain with the indole scaffold. The most active naphthalene inhibitor **3** from the previous report was used as a template upon which the analogous indole inhibitor **2e** and the homologated indole inhibitor **2k** were superimposed. The three most important side chain functional groups in naphthalene inhibitor **3** are considered to be the 6-hydroxy group (H-bond donor and acceptor), the hydrogen from the 3-hydroxy group (H-bond donor), and the side chain hydroxy group (H-bond acceptor) based upon the rational design and SAR for both series of inhibitors. This three point pharmacophore model is identified in both series by asterisks in Scheme 3.

Scheme 3



The "multifit" energy minimization and "fit atoms" facilities within SYBYLTM (6.4, Tripos, St. Louis) were used in sequence to superimpose **2e** and **2k** onto **3**. This overall fitting process was carried out with spring constants (multifit)

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and weights (fit atoms) chosen such that the highest emphasis was on optimally superimposing the scaffold pharmacophore O's and H's (100), followed by the side chain O's (10) and then the intervening amide bond (1). The "multifit" process adjusted the conformations for maximum pharmacophore fit, the subsequent minimization produced the nearest local minimum energy conformations and finally the "fit atoms" process produced the best pharmacophore superimposition of these minimized conformations. As expected, the scaffold pharmacophore O's and H's of both 2e and 2k superimposed closely and similarly upon the corresponding atoms in 3 (all within ca. 0.50 Å). However, the side chain pharmacophore O's of 2e and 2k differed significantly in their superimposition on the corresponding O of 3, with displacements of 1.8 Å vs. only 0.08 Å respectively. This close fit of the three key pharmacophore sites between 2k and 3 provides a rationalization for their potency differing by only a factor of 2.4 (IC₅₀'s 38 μM vs. 16 μM, respectively).

Extending the amide side chain by another carbon atom reduced the activity (2m, 21% vs. 2l, 54%). Adding a methyl group to the benzylic carbon of 2k, in either stereochemistry, greatly reduced the activity (2y, 15% & 2z, 13% vs. 2k, 74%). Replacing the side chain hydroxy group (in the para position) with a carboxylate anion (2n, 0% vs. 2l, 54% and 2p, 7% vs. 2f, 45%) reduced the activity whereas the corresponding methyl esters (2o, 11% & 2q, 32%, respectively) showed a smaller loss of potency. Importantly, replacing the side chain hydroxy group with a fluorine maintained much of the potency (2s, 57% vs. 2k, 74% and 2r, 21% vs. 2e, 30%). Consequently, the fluoro analog 2s has only one hydroxy group left for potential Phase II metabolism (e.g. glucuronide formation), and this remaining hydroxy group is a current target for replacement (Lai et al., 1998).

Using the same method as in the preceding example (Marsilje, 2000), the most potent inhibitor from the current indole series (2k) was analyzed for ATP competition by monitoring the % inhibition at increasing [ATP] while holding the inhibitor concentration constant. Since the [ATP] had little effect on the % inhibition (The % inhibition was 46% and 41% with 2k at 45 μM and [ATP] at 200 μM or 1,000 μM, respectively.), 2k is non-competitive with respect to ATP under these assay conditions.

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In summary, an indole scaffold has been designed, and an initial SAR carried out, for the development of non-ATP competitive pp60^{c-src} inhibitors. The potency of the best indole-based inhibitor from the current series was found to be close to that of the best naphthalene-based inhibitor. The % inhibition was 46% and 41% with 2k at 45 μ M and [ATP] at 200 μ M or 1,000 μ M, respectively.

Example 5 - Synthesis of Additional Indole Derivative Protein Kinase Inhibitors

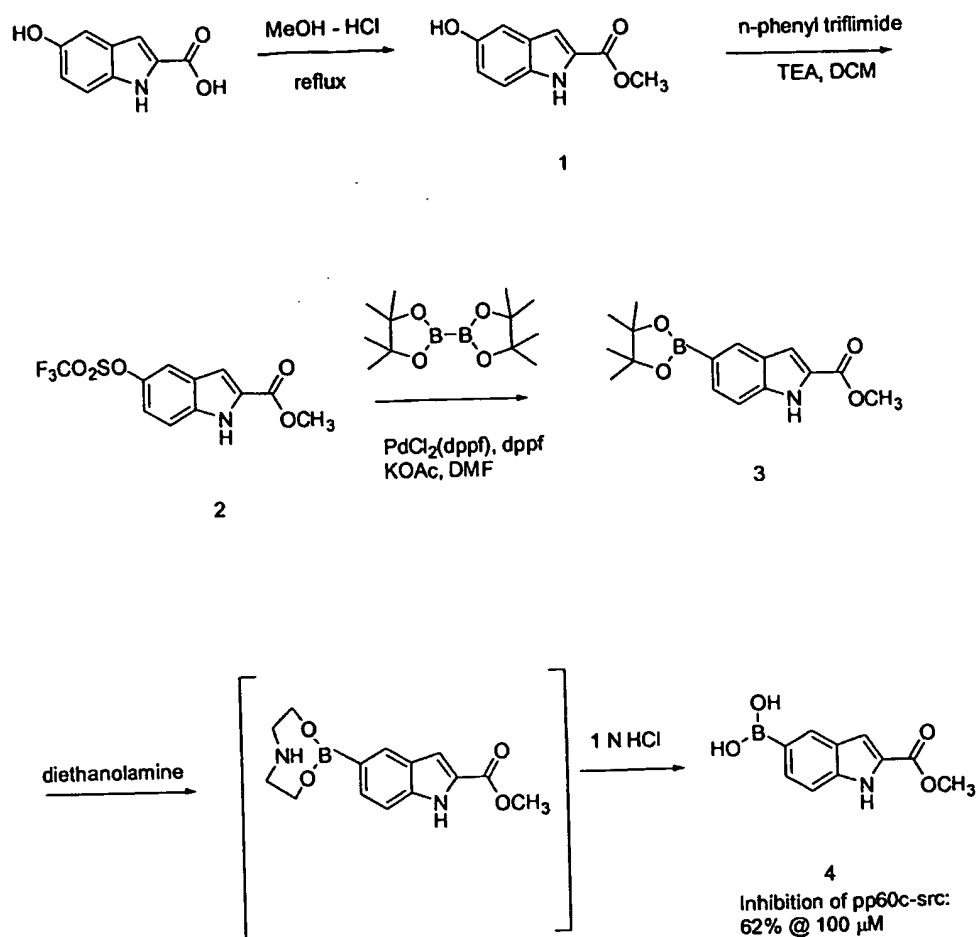
The following results show the synthesis and testing of indole derived protein kinase inhibitors. Four reaction schemes are provided and separately followed by experimental details for the preparation of the final product of each of these reaction schemes. These final products are examples of indole-base tyrosine kinase inhibitors wherein the synthesis with preferred R groups is illustrated (boronic acid, Scheme 1; OH, Scheme 2; an aliphatic amide extension, Scheme 3; and a phosphonic acid Scheme 4).

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Scheme 1

**Methyl 5-hydroxy-2-indolecarboxylate (1)**

Dissolved 3.50 g 5-hydroxy-2-indolecarboxylic acid in anh. MeOH presaturated with

- 5 HCl gas. Refluxed for 48 hours. Concentrated *in vacuo* and triturated with AcCN x3 to remove residual acid. Filtered through silica plug with EtOAc to remove baseline contamination. Recovered 4.32 g (quant. yield) TLC R_f = .78 (EtOAc) ^1H NMR (DMSO- d_6): 3.82 (s, 3H), 6.78 (d, J =8.8 Hz, 1H), 6.88 (s, 1H), 6.93 (s, 1H), 7.23 (d, J =8.8 Hz, 1H), 8.90 (s, 1H) 11.62 (s, 1H) FAB(+) MS m/e 191.9 ($M+1$)

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Methyl 5-[(trifluoromethyl)sulfonyloxy]indole-2-carboxylate (2)

Added 150 ml anh. DCM to 3.24 g (17 mmol) methyl 5-hydroxy-2-indolecarboxylate (1) and 6.67 g (18.7 mmol) n-phenyl trifluoromethane sulfonamide at 0°C. Added 2.6 ml triethylamine dropwise at which point clear yellow solution formed. Stirred at 0°C for 1 hour. Warmed to room temperature and stirred for 2 hours. Concentrated *in vacuo* and purified through silica gel column (1/1 EtOAc/hexanes). Recovered 4.69 g (86%). TLC $R_f = .63$ (1/1 EtOAc/hexanes). HPLC $R_f = 20.879$ 1H NMR (DMSO- d_6): 3.87 (s, 3H), 7.25 (s, 1H), 7.31 (d, $J=9.2$ Hz, 1H), 7.55 (d, $J=9.2$ Hz, 1H), 7.80 (s, 1H), 12.34 s, 1H) FAB(+) MS m/e 323.1 (M+1).

10

Methyl 5-methylindole-2-carboxylate, 4,4,5,5-tetramethyl-1,3,2-dioxaborolanemethyl (3)

500 mg 1.55 mmol methyl 5-[(trifluoromethyl)sulfonyloxy]indole-2-carboxylate (2), 37.9 mg (.05 mmol) $PdCl_2$ (dppf), 432 mg (1.7 mmol) bispinacolatodiboron, 454.8 mg (4.65 mmol) potassium acetate, and 25.7 mg (.05 mmol) dppf were added to a flask and vacuum dried at 40°C for 2 hours. Added 20 ml anh dioxane and heated to 80°C overnight. Reaction turned black as Pd black precipitated out. Filtered off catalyst and ran silica plug to remove baseline impurities. TLC $R_f = .51$ (1/4 EtOAc/Hexane) Crude product was taken through to next reaction.

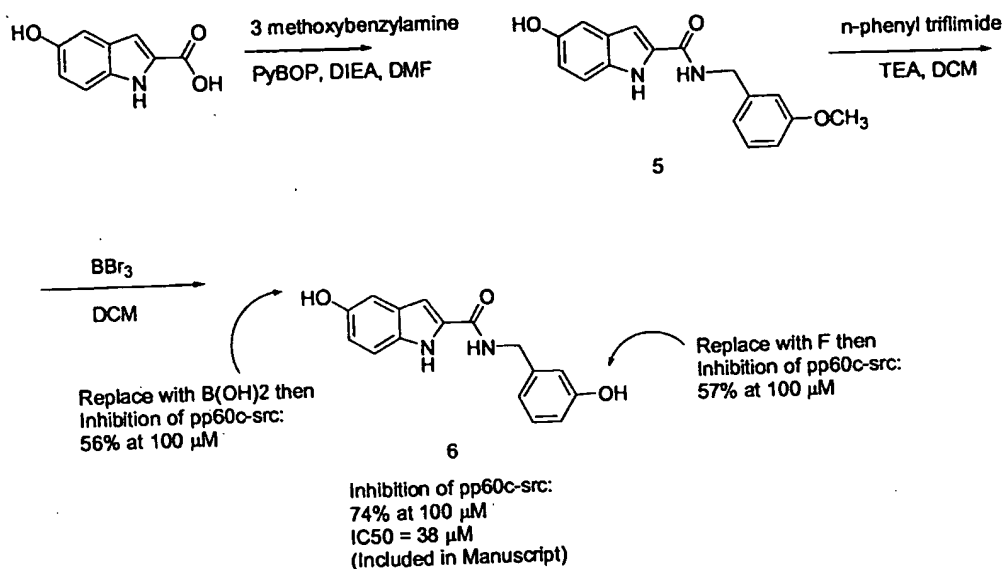
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Methyl 5-boronyl indole-2-carboxylate (4)

391.2 mg (1.3 mmol) methyl 5-methylindole-2-carboxylate, 4,4,5,5-tetramethyl-1,3,2-dioxaborolanemethyl (3) was dissolved in EtOAc. 0.25 ml (2.6 mmol) diethanolamine was added, and the reaction was stirred at room temperature overnight. The white ppt which formed was filtered and sonicated in 1 N HCl. The resulting white ppt was filtered, dissolved in MeOH, and concentrated *in vacuo*. Recovered 36.6 mg (13 %). HPLC $R_f = 13.912$, 1H NMR (DMSO- d_6): 3.85 (s, 3H), 7.15 s, (1H), 7.36 (d, $J=8.4$ Hz, 1H), 7.67 (d, $J=8.4$ Hz, 1H), 7.87 (s, 1H), 8.14 (s, 1H), 11.91 (s, 1H).

30

Scheme 2



Dissolved 2.00g (11.3 mmol) 5-hydroxy-2-indolecarboxylic acid, 1.6 ml (12.4 mmol) 3 methoxybenzylamine, and 5.87 g (11.3 mmol) PyBOP in 10 ml anh. DMF. Cooled to 0°C and added 5.9 ml (33.9 mmol) DIEA. Stirred for 5 minutes at 0°C and allowed to warm to room temperature for 1 hour. Recovered 2.83g (85% yield) TLC $R_f = 0.34$ (1/1 EtOAc / hexanes) 1H NMR (DMSO- d_6): 3.70 (s, 3H), 4.43 (d, $J = 4.4$ Hz, 2H) 6.69 (d, $J = 8.8$ Hz, 1H), 6.78 (d, $J = 7.7$ Hz, 1H), 6.83 (s, 1H), 6.86 (s, 1H), 6.94 (s, 1H), 7.20 (m, 3H), 8.92 (t, $J = 4.4$ Hz, 1H), 11.36 (s, 1H) FAB(+) MS m/e 297.3 (M+1)

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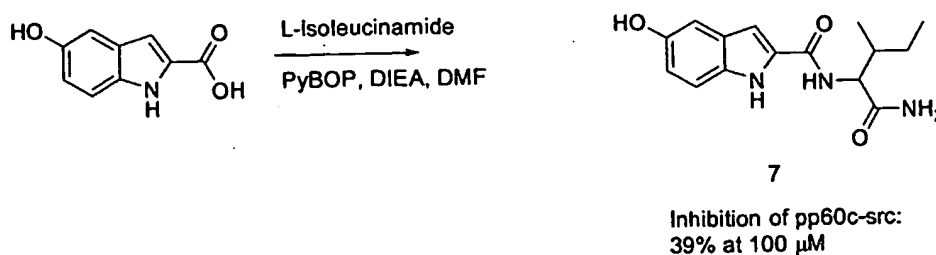
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(5-hydroxyindol-2-yl)-N-[(3-hydroxyphenyl)methyl]carboxamide (6)

- Added 20 ml anh. DCM to 200 mg (0.67 mmol) (5-hydroxyindol-2-yl)-N-[(3-methoxyphenyl)methyl]carboxamide(5) and cooled to -78°C under argon. Added 4.0 ml (4.0 mmol, 6 eq) BBr₃. Held at -78°C for 5 minutes and warmed to rt. After 90 minutes at room temperature, quenched with H₂O and stirred for 10 minutes. Diluted reaction mix with EtOAc and washed with NaHCO₃ and brine. Dried organic layer over MgSO₄ and concentrated *in vacuo*. Ran through silica plug to remove baseline contamination. Recovered X mg. (80% yield.) TLC R_f=0.21 (1/1 EtOAc/hexanes). ¹H NMR (DMSO-d₆): 4.38 (d, J= 4.8 Hz, 2H), 6.59 (d, J=8.8 Hz, 1H), 6.71 (m, 3H) 6.83 (d, J=1.8 Hz, 1H), 6.94 (s, 1H), 7.08 (dd, J= 7.7 Hz, 1H), 7.19 (d, J=8.8 Hz, 1H), 8.84 (t, J=5.9 Hz), 11.28, (s, 1H). FAB(+) MS m/e 283.2 (M+1)

Scheme 3

**15 N-(1-carbamoyl-2-methylbutyl)(5-hydroxyindol-2-yl)carboxamide (7)**

- 100 mg (0.56 mmol) 5-hydroxy-2-indolecarboxylic acid, 103.4 mg (0.62 mmol, 1.1 eq) L-isoleucinamide, and 291 mg (0.56 mmol, 1 eq) PyBOP were all dissolved in 1 ml anh DMF. The solution was cooled to 0° C and 0.3 ml (1.68 mmol, 3 eq) DIEA was added. The reaction mixture was stirred for 1 minute at 0° C and at room temperature for 1 hour. The reaction was then diluted with EtOAc and washed with 1 N HCl x3 and satd NaHCO₃ x 3. The organic layer was dried over MgSO₄, and concentrated *in vacuo* to give 166.7 mg (91 % yield.) TLC R_f=0.08 (1/1 EtOAc/hexanes). ¹H NMR (DMSO-d₆): 0.83 (m, 6H), 1.15 (m, 2H), 1.68 (m, 1H), 1.83 (m, 1H), 4.29 (t, J=8.8 Hz, 1H), 6.69 (d, J=8.5 Hz, 1H), 6.83 (s, 1H), 7.01, (s,

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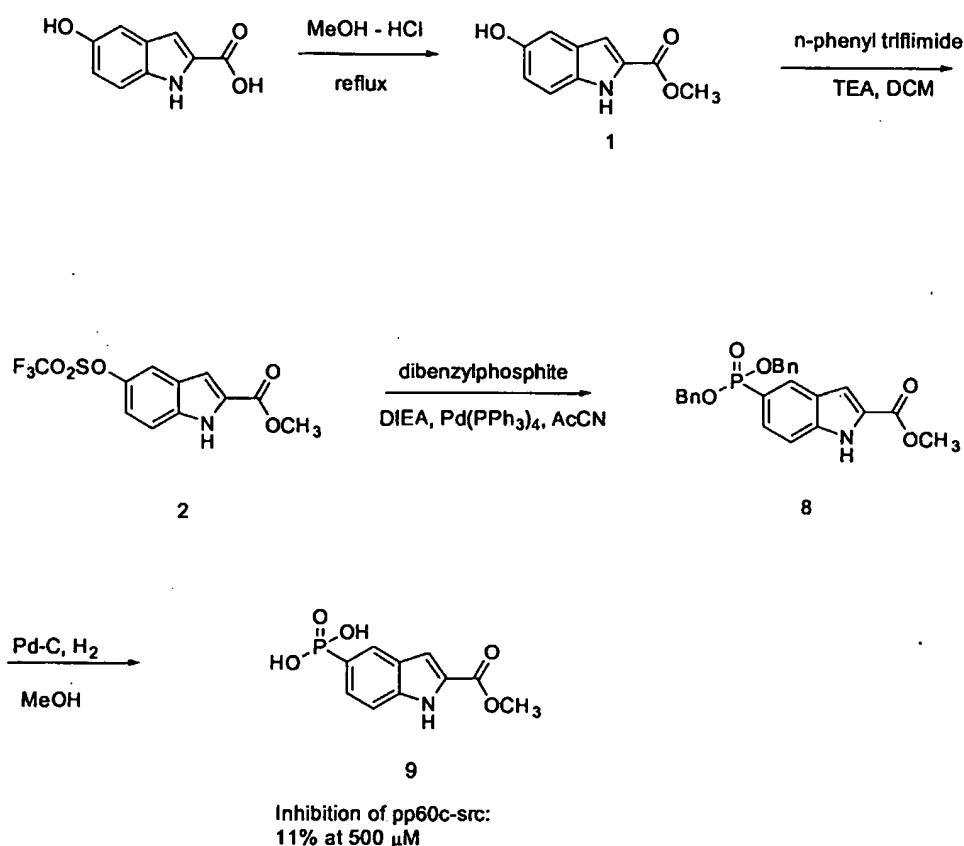
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1H), 7.06 (s, 1H), 7.19 (d, J=8.4 Hz, 1H), 7.48, (s, 1H), 8.00 (d, 9.2 Hz, 1H), 8.76 (s, 1H), 11.3, (s, 1H). FAB(+) MS m/e 290.1 (M+1)

Scheme 4

5



Methyl 5-dibenzylphosphorylindole-2-carboxylate (8)

200 mg (0.62 mmol) methyl 5-[(trifluoromethyl)sulfonyl]indole-2-carboxylate (2), 195.8 mg (.74 mmol, 1.2 eq) dibenzylphosphite, 0.14 ml (0.81 mmol, 1.3 eq) DIEA, and 35.7 mg (0.03 mmol, 5 mol %) Pd(PPh₃)₄ were all dissolved in anhydrous AcCN under argon. The reaction mixture was heated to 80°C overnight. The solvent was removed under reduced pressure, and the title compound was isolated by silica gel

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chromatography. 130 mg (50% yield). TLC R_f =0.28 (1/1 EtOAc/hexanes) ^1H NMR (DMSO- d_6): 3.85 (s, 3H), 4.98-5.01 (m, 4H), 7.28-7.32 (m, 11H), 7.53-7.55 (m, 2H), 8.17 (d, J =14.6 Hz, 1H) ^{31}P NMR (DMSO- d_6): 23.89.

5 Methyl 5-phosphonolindole-2-carboxylate

Methyl 5-dibenzylphosphorylindole-2-carboxylate (8) (125 mg) was dissolved in 10 ml MeOH. 20 mg Pd-C was added and the mixture was hydrogenated in a Parr apparatus overnight. Filtered off catalyst and removed solvent under reduced pressure. Obtained 72.5 mg (73% yield). TLC R_f = baseline in EtOAc. ^1H NMR (DMSO- d_6): 3.84 (s, 3H), 7.24 (s, 1H), 7.44-7.49 (m, 2H), 8.01 (d, J =14.3 Hz, 1H) 12.11 (s, 1H) ^{31}P NMR (DMSO- d_6): 17.22.

The ester compounds in this example could be increased in potency by converting the ester to an amide and/or adding additional specificity elements.

15

Example 6 – Synthesis of Further Indole Derivative Protein Kinase Inhibitors

The synthesis of some further elaborated indole inhibitors is illustrated in below. These syntheses could result in compounds with greater potency against pp60c-src and other tyrosine kinases. The methyl ester group can be subsequently converted into various amide derivatives to increase potency.

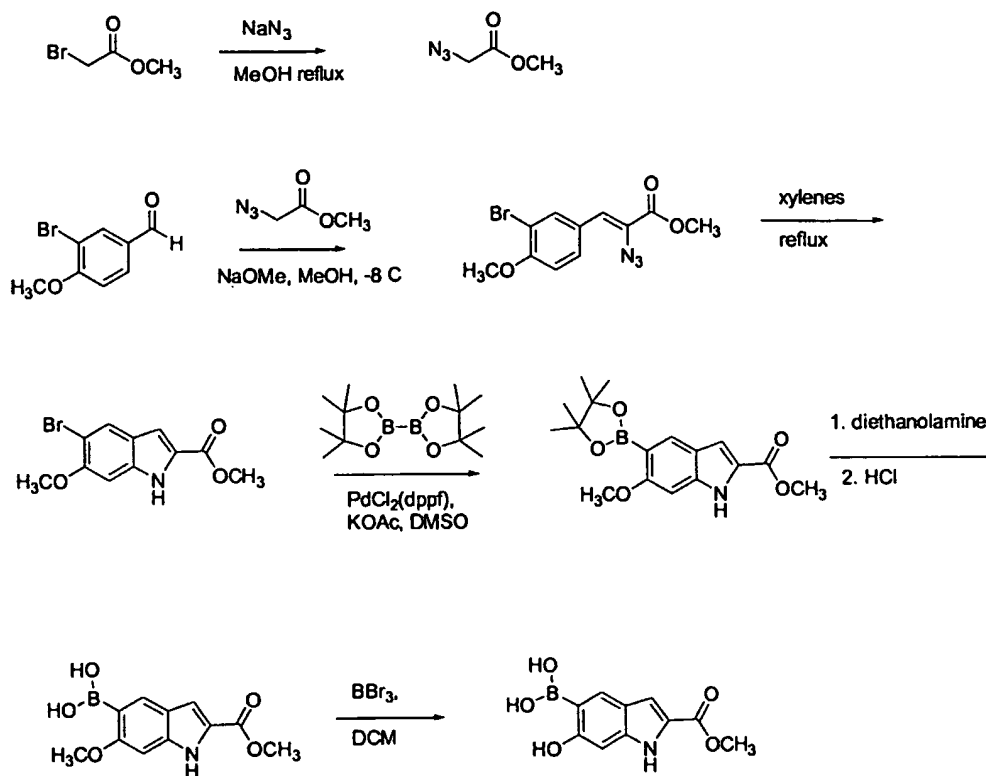
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Scheme 1:

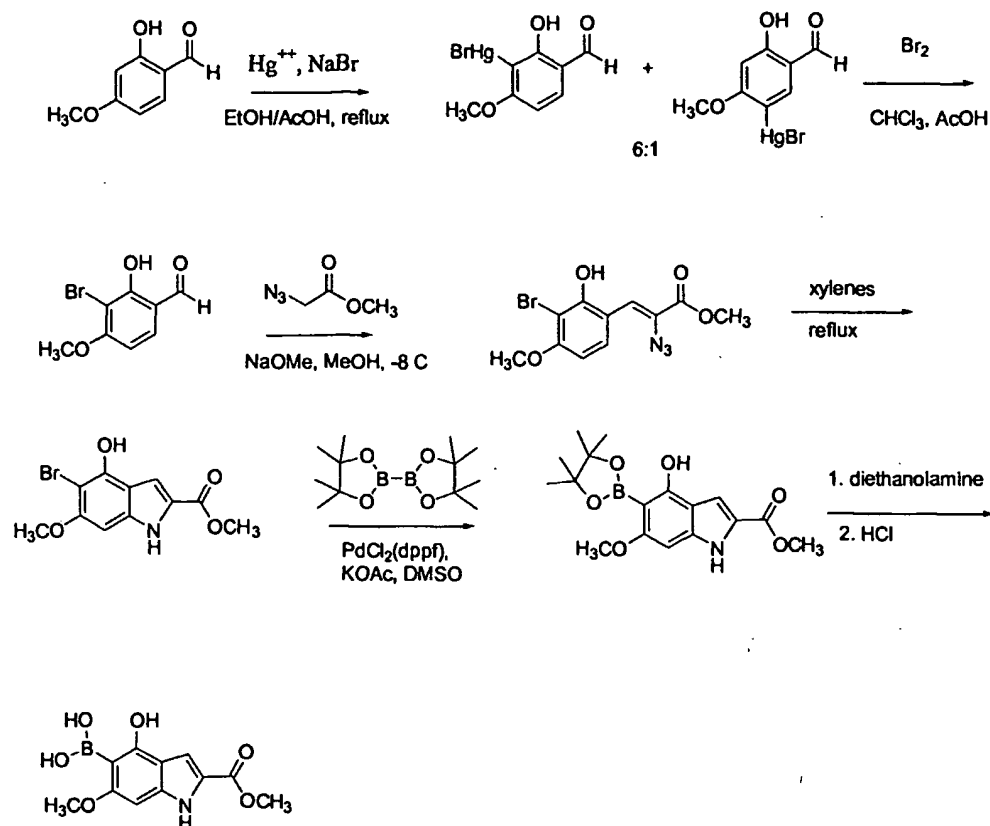


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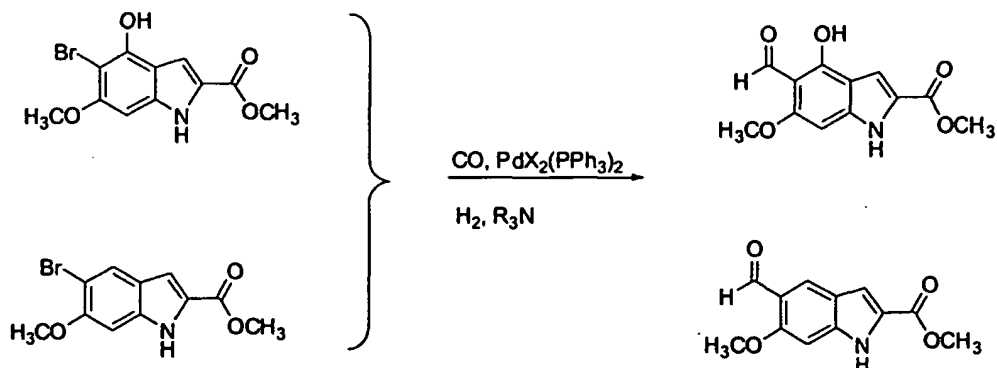
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Scheme 2:



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Scheme 3:



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Example 7 – Toxicity of Src inhibitors

There is considerable recent literature support for targeting pp60^{c-src} (Src) as a broadly useful approach to cancer therapy without resulting in serious toxicity. For example, tumors that display enhanced EGF receptor PTK signaling, or overexpress the related Her-2/neu receptor, have constitutively activated Src and enhanced tumor invasiveness. Inhibition of Src in these cells induces growth arrest, triggers apoptosis, and reverses the transformed phenotype (Karni et al., 1999). It is known that abnormally elevated Src activity allows transformed cells to grow in an anchorage-independent fashion. This is apparently caused by the fact that extracellular matrix signaling elevates Src activity in the FAK/Src pathway, in a coordinated fashion with mitogenic signaling, and thereby blocks an apoptotic mechanism which would normally have been activated. Consequently FAK/Src inhibition in tumor cells may induce apoptosis because the apoptotic mechanism which would have normally become activated upon breaking free from the extracellular matrix would be induced (Hisano et al., 1997). Additionally, reduced VEGF mRNA expression was noted upon Src inhibition and tumors derived from these Src-inhibited cell lines showed reduced angiogenic development (Ellis et al., 1998).

The issue of potential toxicity of Src inhibition has been addressed with very promising results. For example, a knock-out of the Src gene in mice led to only one defect, namely osteoclasts that fail to form ruffled borders and consequently do not resorb bone. However, the osteoclast bone resorb function was rescued in these mice by inserting a kinase defective Src gene (Schwartzberg et al., 1997). This suggested that Src kinase activity can be inhibited *in vivo* without triggering the only known toxicity because the presence of the Src protein is apparently sufficient to recruit and activate other PTKs (which are essential for maintaining osteoclast function) in an osteoclast essential signaling complex.

Src has been proposed to be a “universal” target for cancer therapy since it has been found to be overactivated in a growing number of human tumors, in addition to those noted above (Levitzki, 1996). The potential benefits of Src inhibition for cancer therapy appear to be four-fold based upon the cited, and additional, literature. They are: 1) Inhibition of uncontrolled cell growth caused by autocrine growth factor loop

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effects, etc. 2) Inhibition of metastasis due to triggering apoptosis upon breaking free from the cell matrix. 3) Inhibition of tumor angiogenesis via reduced VEGF levels. 4) Low toxicity.

The initial non-peptide Src inhibitors have also shown very encouraging results in four different series of cell culture assays. 1) In the NIH 60-tumor cell panel assay, broad activity (as one would expect for a Src inhibitor) was seen against the tumor cell lines, including the prostate lines. For example, three of the inhibitors gave the following growth inhibition IC_{50} 's against the NIH prostate cancer cell lines: 45 (PC-3, 15 μ M; DU-145, 38 μ M), 43-meta (PC-3, 19 μ M), 49-meta (PC-3, 39 μ M; DU-145, > 100 μ M). 2) In the v-Src transformed normal rat kidney cell line (LA25) 43-meta and 45 specifically blocked the v-Src induced cell growth without inhibiting the normal growth of the parent non-transformed cells. This result showed that the inhibitors do not affect normal cells but are effective in blocking Src induced cell transformation. 3) The Src inhibitors were compared to the cancer drugs etoposide, taxol, doxorubicin and cisplatin in ovarian tumors from three different patients and an abdominal carcinoma from another patient. In all cases, the Src inhibitors were at least as effective, and typically more effective, than the known cancer drugs, with full efficacy seen at the lowest dose tested (3 μ M). As a representative example, a comparison of taxol and doxorubicin (they were more effective than etoposide & cisplatin in this particular tumor cell culture) with the three Src inhibitors mentioned above (structures shown in Figure 16E) utilizing ovarian tumor cells from tumor N015 is shown in Figure 16A. 4) The Src inhibitors were also tested for inhibition of normal human fibroblast cell growth and found no inhibition of normal cell growth (both subconfluent and confluent; some enhanced growth was observed instead), indicating that these inhibitors are not toxic to normal cells even at a 10-fold higher concentration. An example of his data is given in Figure 16B. 5) Two of the Src inhibitors were also tested for inhibition of *ts* v-Src stimulated LA25 cell growth. The results are shown in Figure 16C. These results show that the tested compounds inhibit Src stimulated cell growth. 6) Two of the Src inhibitors were also tested for inhibition of normal rat kidney cell growth. The results are shown in Figure 16D and illustrate that the inhibitors are cytoprotective for normal cells.

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Overall, the cell data obtained thus far shows what one might expect for Src inhibitors, i.e. broad activity against many cancer cell lines with little or no normal cell toxicity.

The preliminary Src inhibitors are lead structures from which it is possible to design more potent and selective inhibitors. In addition to utilizing the tyrosine kinase crystal structures, molecular modeling studies can be carried out with the natural product tyrosine kinase inhibitor damnacanthal (Faltynek et al., 1995) to investigate its peptide-competitive binding mode. These additional modeling studies are enable one to design further analogs of Src inhibitors wherein the key pharmacophore elements of damnacanthal are incorporated into the new inhibitors. Their syntheses will be undertaken and the isolated Src testing done as reported (Marsilje 2000).

Example 8 - Development of Src PTK Inhibitors for Treatment of Malignant Prostate Cancer

Prostate cancer cells have been reported to have both an overexpression of paxillin and p130cas as well as being hyperphosphorylated (Tremblay et al., 1996) and may thus be a prime target for Src inhibitors. Prostate cancer is the most frequent malignancy and the second leading cause of cancer mortality among men. When clinically localized, it is most effectively treated by surgery or radiation therapy (Dorkin et al., 1997). For advanced disease, androgen suppression has been a mainstay of therapy for several decades and is known to cause cessation of cellular growth and stimulation of apoptosis in androgen-responsive prostate cancer cells (Dorkin et al., 1997). However, because prostate cancer is composed of a heterogeneous cell population, disease progression and mortality ultimately results from the emergence of androgen-independent cells since there is no treatment for advanced prostate cancer (Abate-Shen et al, 2000). Identification of potent inhibitors of PTKs active against highly malignant prostate cancer would provide a valuable tool in the treatment of advanced disease.

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Methodology

Apoptosis- Media from controls and drug treated cells was transferred to a 30 ml tube and kept on ice. Adherent cells were gently washed with PBS and trypsinized for 3 minutes at 37°C. Trypsinized cells were combined with floating cells and counted. Cells (5×10^5) were transferred to a 15 ml conical tube and washed once with 5 ml cold PBS and resuspended with Annexin V-FITC in binding buffer for 15 minutes in the dark. Cells were then centrifuged, resuspended in binding buffer, and 10 μ l of propidium iodide was added. Analysis was done by FACSCAN. Cells Annexin-labeled were considered apoptotic. Dead cells were labeled with propidium iodide and live cells were unlabeled. Results were confirmed by immunohistochemistry.

Western blotting analysis- Total proteins were isolated from $\sim 5 \times 10^6$ cells and lysed in 1 ml of lysing buffer [50 mM Tris-HCl, pH 8.0, 100 mM NaCl, 0.5% sodium dodecyl sulfate (SDS), 0.5% sodium deoxycholate, 0.5% Nonidet P40, 10 mM dithiothreitol, 1 mM PMSF and 0.4U aprotinin]. Protein concentrations were determined with a DC protein assay kit. Expression of tyrosine phosphorylated proteins was investigated by immunoblotting. Protein from the cell lysates (50 μ g) was subjected to a 10% SDS-polyacrylamide gel electrophoresis followed by transfer onto a 4.5- μ m Trans-Blot Transfer Medium using a nitrocellulose membrane. The blots were incubated with the appropriate secondary antibody and developed using a chemiluminescence reagent kit. Westerns obtained for paxillin were obtained by using standard stripping and reprobing of the membrane with a new secondary antibody. Each blot is typical of multiple runs.

Toxicity Assay- The sulforhodamine assay is designed to measure cell viability in a 96-well plate format. Cells were counted and plated at a concentration of 50,000 cells/well in 0.1 mL of 10% FBS in RPCI 1640 media. Plates were grown for 2 days in order to allow cells to attach and were then treated with an increasing concentration of drug for 72 hours. The media was removed from the wells and the plates fixed for 1 hour with 10% trichloroacetic acid. The wells were washed with PBS and stained with 0.4% sulforhodamine B for 15 minutes. Unbound dye was then removed by washing the plates with a 1% acetic acid solution, and (protein) bound

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dye was extracted using 10mM Tris. The absorbance was then measured in a multi-well plate reader at wavelength of 570nm. Each point is the average of 12 points \pm S.D. and each graph is representative of multiple analyses.

5 Results

A considerable amount of data for Src inhibitors in highly malignant prostate cancer cells has been obtained. Representative toxicity data is shown (Figures 17A and B) following 72 hours of continuous exposure of each of four drugs and one inactive control. Determination of time course and apoptotic response has been performed primarily using 45 (data not shown) and 45 has been identified as the most active compound against highly malignant PC3-LN3 prostate cancer cells (Figures 17A and B). A second analysis using malignant LNCaP-LN cells showed nearly equal potency of the two compounds 45 and 49-meta (data not shown). KLM2-25 is a negative control and shows little activity in either cell line. The apoptotic response to this compound was unusual in that only a small percentage of cells (less than 5%) underwent apoptosis at any given time using an LD50 concentration. However, a 20% apoptotic rate was observed using an LD90 concentration for 92 hours (data not shown). Furthermore, 45 has been shown to be a good inhibitor of tyrosine kinase activity, although it lacks specificity for any single kinase target (Figure 18A). Stripping the antibodies from the blotted membranes and re-blotting with a second antibody for either paxillin (Figure 18B) or p130^{cas} (not shown) has resulted in the successful identification of two of the affected protein bands in the Western blots. Re-probing with a second antibody provides unequivocal identification of individual protein bands due to the strict identification with the same molecular size labels. While 45 has since been characterized as having a short *in vivo* half-life, it has been most useful in developing a comprehensive strategy for evaluating these compounds *in vitro*.

Subsequently, two distinct phosphorylated substrates for focal adhesion kinase (paxillin and p130 cas) and a third unknown substrate were quantitated. Quantitation was done by densitometry scanning of the film of the Western blots and is shown in Figure 19. All three phosphorylated substrates showed a dose-dependent inhibition of phosphorylation.

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Example 9 – Protection Against Noise-Induced Hearing Loss Using PTK Inhibitors

5 Chinchillas (N=8) were used in studies of noise-induced hearing loss. The animals' hearing sensitivity was measured using standard electrophysical techniques before the experimental manipulation. In particular, hearing thresholds were measured through evoked potentials from recording electrodes chronically implanted in the inferior colliculus, following standard laboratory procedures. Animals were
10 anesthetized, the auditory bullae were opened, and the left and right cochleas were visualized. The round window leading to the scala tympani of the cochlea was used as the access point for drug application. Four animals were treated with 30 μ l of 3 mM 45, emulsified in DMSO, to 1000 mM of saline solution, which was placed on the round window of one ear, and a control solution of 3 mM DMSO to 1000 mM of
15 saline solution, which was placed on the round window of the other ear. Five animals were treated with 30 μ l of 3 mM 1a (from Table VI in Example 1), emulsified in DMSO, to 1000 mM of saline solution, which was placed on the round window of one ear, and a control solution of 3 mM DMSO to 1000 mM of saline solution, which was placed on the round window of the other ear (one animal was lost prior to the end
20 of the experiments). In each case, the solution was allowed to set on the round window for 30 minutes, then the auditory bullae were closed. Subsequently, the animals were exposed to 4 kHz band noise at 105 dB SPL for four hours. Following the noise exposure, the animals' hearing was tested at day 1, day 3, day 7, and day 20 to determine evoked potential threshold shifts. Permanent threshold shift was
25 assessed at day 20. The cochleas were harvested at day 20 to allow for morphological examination of the cochleas. Data for 45 is shown in Tables XI-XIII and data for 1a (Ex. 1) is shown in Table XIV, below.

TABLE XI

30

Pretest	0.5kHz	1kHz	2kHz	4kHz	8kHz
Control	20	20	15	15	15
	25	20	25	20	10
Control	22.5	20	20	17.5	12.5
<u>45</u>	25	25	20	15	10

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	30	30	30	20	10
45	27.5	27.5	25	17.5	10
45 - 6778	0.5kHz	1kHz	2kHz	4kHz	8kHz
Day 0	55	70	75	85	80
Day 1	35	30	65	75	75
Day 3	15	5	40	45	60
Day 20	5	5	25	30	0
Control 6778	0.5kHz	1kHz	2kHz	4kHz	8kHz
Day 0	60	75	80	80	75
Day 1	45	40	75	75	75
Day 3	10	10	50	55	55
Day 20	5	10	40	35	25
45 - 6679	0.5kHz	1kHz	2kHz	4kHz	8kHz
Day 0	55	60	65	75	75
Day 1	30	50	60	70	75
Day 3	20	25	40	55	45
Day 20	-5	0	10	23	-5
Control 6679	0.5kHz	1kHz	2kHz	4kHz	8kHz
Day 0	55	70	70	75	80
Day 1	40	60	65	70	80
Day 3	35	60	65	75	80
Day 20	0	10	25	35	10
Control	0.5kHz	1kHz	2kHz	4kHz	8kHz
Day 0	55	70	70	75	80
Day 0	70	75	80	80	75
Average Day 0	57.5	72.5	75	77.5	77.5
Day 1	40	60	65	70	80
Day 1	45	40	75	75	75
Average Day 1	42.5	50	70	72.5	77.5
Day 3	35	60	65	75	80
Day 3	10	10	50	55	55
Average Day 3	22.5	35	57.5	65	67.5
Day 20	0	10	25	35	10
Day 20	5	10	40	35	25
Average Day 20	2.5	10	32.5	35	17.5
45	0.5kHz	1kHz	2kHz	4kHz	8kHz
Day 0	55	70	75	85	80

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Day 0	55	60	65	75	75
Average day 0	55	65	70	80	77.5
Day 1	35	30	65	75	75
Day 1	30	50	60	70	75
Average Day 1	32.5	40	62.5	72.5	75
Day 3	15	5	40	45	60
Day 3	20	25	40	55	45
Average Day 3	17.5	15	40	50	52.5
Day 20	5	5	25	30	0
Day 20	-5	0	10	23	-5
Average Day 20	0	2.5	17.5	26.5	-2.5
	0.5kHz	1kHz	2kHz	4kHz	8kHz
Control Day 0	57.5	72.5	75	77.5	77.5
<u>45</u> Day 0	55	65	70	80	77.5
Control Day 1	42.5	50	70	72.5	77.5
<u>45</u> Day 1	32.5	40	62.5	72.5	75
Control Day 3	22.5	35	57.5	65	67.5
<u>45</u> Day 3	17.5	15	40	50	52.5
Control Day 20	2.5	10	32.5	35	17.5
<u>45</u> Day 20	0	2.5	17.5	26.5	-2.5
	0.5kHz	1kHz	2kHz	4kHz	8kHz
Control Day 0	57.5	72.5	75	77.5	77.5
Control Day 1	42.5	50	70	72.5	77.5
Control Day 3	22.5	35	57.5	65	67.5
Control Day 20	2.5	10	32.5	35	17.5
<u>45</u> Day 0	55	65	70	80	77.5
<u>45</u> Day 1	32.5	40	62.5	72.5	75
<u>45</u> Day 3	17.5	15	40	50	52.5
<u>45</u> Day 20	0	2.5	17.5	26.5	-2.5
	0.5kHz	1kHz	2kHz	4kHz	8kHz
<u>45</u> Day 20	0	2.5	17.5	26.5	-2.5
Control Day 20	2.5	10	32.5	35	17.5

TABLE XII

45 - 6696	0.5kHz	1kHz	2kHz	4kHz	8kHz
day 0	38	50	70	75	80
day 1	27	20	70	75	65
day 3	10	15	55	53	55

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day 7	13	10	45	50	50
day 20					
Control 6696	0.5kHz	1kHz	2kHz	4kHz	8kHz
day 0	35	45	75	80	90
day 1	30	40	75	80	80
day 3	7	15	50	60	70
day 7	5	15	45	50	60
day 20					
45 - 6698	0.5kHz	1kHz	2kHz	4kHz	8kHz
day 0	30	45	65	70	80
day 1	0	15	45	65	60
day 3	-5	5	25	40	40
day 7	-5	5	25	25	0
day 20	-5	0	0	0	-5
Control 6698	0.5kHz	1kHz	2kHz	4kHz	8kHz
day 0	55	40	65	70	80
day 1	10	15	45	60	70
day 3	15	15	45	40	55
day 7	5	5	25	35	10
day 20	10	10	20	30	5
45 - 6699	0.5kHz	1kHz	2kHz	4kHz	8kHz
day 0	70	65	70	75	85
day 1	60	65	70	75	85
day 3	25	20	70	70	75
day 7	10	5	45	40	45
day 20	10	10	45	40	45
Control 6699	0.5kHz	1kHz	2kHz	4kHz	8kHz
day 0	70	70	65	70	85
day 1	60	70	65	70	85
day 3	50	65	60	65	70
day 7	38	55	50	45	65
day 20	28	35	50	45	60

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Pretest	0.5kHz	1kHz	2kHz	4kHz	8kHz
Controls	25	25	30	25	10
	25	30	30	25	15
Controls	25	27.5	30	25	12.5
45	35	30	30	25	15
	25	30	25	20	10
45	30	30	27.5	22.5	12.5

TABLE XIII

0.5kHz	Control	45
day 0	62.5	50
day 1	35	30
day 3	32.5	10
day 7	21.5	2.5
day 20	19	2.5
1kHz	Control	45
day 0	55	55
day 1	42.5	40
day 3	40	12.5
day 7	30	5
day 20	22.5	5
2kHz	Control	45
day 0	65	67.5
day 1	55	57.5
day 3	52.5	47.5
day 7	37.5	35
day 20	35	22.5
4kHz	Control	45
day 0	70	72.5
day 1	65	70
day 3	52.5	55
day 7	40	32.5
day 20	37.5	20
8kHz	Control	45
day 0	82.5	82.5
day 1	77.5	72.5
day 3	62.5	57.5
day 7	37.5	22.5
day 20	32.5	20

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TABLE XIV

Pretest	0.5kHz	1kHz	2kHz	4kHz	8kHz
Control 6821	30	20	25	15	7.5
Control 6845	30	25	20	15	10
Control 6850	27	25	15	10	0
Control 6828	20	15	20	5	5
Control 6829	20	20	20	20	5
Control	25.4	21	20	13	5.5
1a 6821	30	22.5	25	20	10
1a 6845	35	25	25	10	0
1a 6850	25	25	10	12	0
1a 6828	20	25	15	5	0
1a 6829	23	25	25	15	10
1a	26.6	24.5	20	12.4	4
Day 1	0.5kHz	1kHz	2kHz	4kHz	8kHz
Control 6821	5	25	50	60	72.5
Control 6845	15	15	40	75	80
Control 6850	8	10	25	65	55
Control 6828	5	20	55	75	80
Control Day 1	8.25	17.5	42.5	68.75	71.875
ctrlsd	4.716991	6.454972	13.22876	7.5	11.79248
1a 6821	0	2.5	0	10	0
1a 6845	5	20	25	35	30
1a 6850	10	0	20	68	35
1a 6828	0	5	55	55	25
1a Day 1	3.75	6.875	25	42	22.5
	4.787136	8.984941	22.7303	25.28504	15.54563
Day 3	0.5kHz	1kHz	2kHz	4kHz	8kHz
Control 6821	10	25	50	55	67.5
Control 6845	10	15	35	55	45
Control 6850	3	5	15	25	15
Control 6828	5	15	40	65	55
Control 6829	20	20	35	45	45
Control Day 3	9.6	16	35	49	45.5
	6.580274	7.416198	12.74755	15.16575	19.39716
1a 6821	5	7.5	0	10	0
1a 6845	5	5	0	0	15
1a 6850	5	2	15	25	15
1a 6828	0	0	40	55	0
1a 6829	12	20	35	45	45
1a Day 3	5.4	6.9	18	27	15
	4.27785	7.861298	18.90767	23.07596	18.37117

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Day 7	0.5kHz	1kHz	2kHz	4kHz	8kHz
Control 6821	0	10	20	20	45
Control 6845	10	15	25	45	45
Control 6850	6	5	15	30	10
Control 6828	10	20	37	65	60
Control 6829	20	25	45	40	55
Control Day 7	9.2	15	28.4	40	43
	7.293833	7.905694	12.36123	16.95582	19.55761
1a 6821	0	0	0	0	0
1a 6845	5	15	0	5	20
1a 6850	8	0	15	15	0
1a 6828	15	0	40	55	30
1a 6829	12	15	20	45	40
1a Day 7	8	6	15	24	18
	5.87367	8.215838	16.58312	24.59675	17.888854
Day 20	0.5kHz	1kHz	2kHz	4kHz	8kHz
Control 6821	0	10	25	35	7.5
Control 6845	0	5	25	45	40
Control 6850	8	0	10	20	10
Control 6829	15	20	30	30	18
Control Day 20	5.75	8.75	22.5	32.5	18.875
	7.228416	8.539126	8.660254	10.40833	14.77822
1a 6821	0	0	0	0	-5
1a 6845	0	0	0	0	5
1a 6850	5	0	15	11	0
1a 6829	7	5	10	25	15
1a Day 20	3	1.25	6.25	9	3.75
	3.559026	2.5	7.5	11.80603	8.539126
	0.5kHz	1kHz	2kHz	4kHz	8kHz
Control Day 1	8.25	17.5	42.5	68.75	71.875
Control Day 3	9.6	16	35	49	45.5
Control Day 7	9.2	15	28.4	40	43
Control Day 20	5.75	8.75	22.5	32.5	18.875
1a Day 1	3.75	6.875	25	42	22.5
1a Day 3	5.4	6.9	18	27	15
1a Day 7	8	6	15	24	18
1a Day 20	3	1.25	6.25	9	3.75

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Figures 20-26 show the average threshold shifts for animals treated with 45. In particular, Figure 20 shows average threshold shifts after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise tested prior to experimental manipulation (i.e., exposure to 4 kHz band noise at 105 dB for four hours). Figure 21 shows
5 average threshold shifts after exposure to 0.5 kHz band noise at day 0, day 1, day 3, and day 20 after experimental manipulation. Figure 22 shows average threshold shifts after exposure to 1 kHz band noise at day 0, day 1, day 3, and day 20 after experimental manipulation. Figure 23 shows average threshold shifts after exposure to 2 kHz band noise at day 0, day 1, day 3, and day 20 after experimental
10 manipulation. Figure 24 shows average threshold shifts after exposure to 4 kHz band noise at day 0, day 1, day 3, and day 20 after experimental manipulation. Figure 25 shows average threshold shifts after exposure to 8 kHz band noise at day 0, day 1, day 3, and day 20 after experimental manipulation. Figure 26 shows the average dB threshold shift at day 20 for control and treated ears. As shown in Figures 21-26 the
15 average dB threshold shifts for treated ears were lower, indicating less hearing loss.

Figures 27-32 show the average threshold shifts for animals treated with 1a (from Table VI in Example 1). In particular, Figure 27 shows average threshold shifts after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise tested prior to experimental manipulation. Figure 28 shows average threshold shifts after exposure
20 to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise on day 1 after experimental manipulation. Figure 29 shows average threshold shifts after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise on day 3 after experimental manipulation. Figure 30 shows average threshold shifts after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise on day 7 after experimental manipulation. Figure 31
25 shows average threshold shifts after exposure to 0.5 kHz, 1 kHz, 2 kHz, 4 kHz, and 8 kHz band noise on day 20 after experimental manipulation. Figure 32 shows average threshold shifts after exposure to 8000 Hz on day 1, day 3, day 7, and day 20. As shown in Figures 28-32, the average dB threshold shifts for treated ears were lower, indicating less hearing loss.

30 As shown in Figures 20-32, both 45 and 1a (Ex. 1) provided protection against the noise exposure. However, 1a (Ex. 1) provided the greatest level of protection. In particular, the PTK inhibitor treated ears had, on average, 15 to 25 dB less hearing

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loss than the control ears and the animals showed no side effects of the experimental manipulation.

5 **Example 10 – Inhibition of Noise-Induced Apoptosis in Cochlear Hair Cells
Using Inhibitors of the PTKs**

Chinchillas (N=3) were exposed to 75-pairs of impulse noise at 155 dB pSPL. The animals were sacrificed 5 minutes after the noise exposure. The cochleas were examined for activation of the focal adhesion complex using an antibody against focal
10 adhesion kinase, which is an intrinsic member of the complex.

Figures 33A-F show the effect of high level impulse noise on chinchilla cochleas without treatment with a PTK inhibitor. In particular, Figure 33A is an electron micrograph which shows the cochlear damage following high level impulse noise (155 dB). Figure 33A shows a split at the reticular lamina (S). The split
15 appears to be between the second and third rows of outer hair cells. Figure 33B depicts a cochlea stained immunohistochemically for focal adhesion kinase (FAK) following a moderately high level octave band noise (105 dB). The staining observed in Figure 33B is relatively low level and approximates that observed without noise. The staining appears to be localized primarily at the pharyngeal processes of the
20 Deiter cells and not at the hair cells. Upon elevating the noise level to 110 dB OBN, apoptotic cells appeared, as shown in Figure 33C. These apoptotic cells are located in two regions of the upper left quadrant of the figure and the nuclei appear bright and highly condensed, whereas the normal nuclei are large and more diffuse in color. Figure 33D is a photo of the same cells stained with focal adhesion kinase (FAK)
25 antibody (as in Figure 33B; however, here the pharyngeal processes appear to surround a lesion where cells are missing). These lesions correspond to the areas in Figure 33C where the cells underwent apoptosis. Figure 33E shows the same region but at a lower vertical plane, demonstrating that the lesion extends well below the cuticular plate and into the cell body. Figure 33F shows cochleas exposed to impulse
30 noise at 155 dB SPL. The cochleas lost their integrity at the cuticular plate and were heavily stained throughout. Many dark areas are seen, which represent areas where hair cells have died.

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Figures 34A shows a cochlea pretreated with 1a (Ex. 1), whereas Figure 34B shows an untreated cochlea following exposure to high level noise (155 dB). In the treated cochlea (Figure 34A), there is a high level of FAK staining that extends beyond the pharyngeal processes of the Deiter cells and well into the cuticular plate.

5 The punctate nature of the staining is indicative of the formation of focal adhesion complexes of which FAK is an intrinsic member. Furthermore, the three rows of hair cell nuclei (labeled OHC1-3) appear both in order and intact and without any indication of apoptosis taking place. Since FAK is known to be active within focal adhesion complexes, this data strongly suggests that FAK is active following a high

10 noise exposure. It is hypothesized that it is the inhibition of the kinase function that is prevented through the treatment with 1a (Ex. 1) and results in the survival of cochlear hair cells.

In contrast to Figure 34A, Figure 34B demonstrates a somewhat lower level of FAK staining, but also shows a remarkably high level of cell death. In this figure,

15 nearly half of the cells have died by apoptosis, as indicated by the number of condensed nuclei. This contrasts with Figure 34A, where no apoptotic nuclei were observed with treatment. Since 1a (Ex. 1) can inhibit phosphorylation of several FAK substrates, including paxillin and pp130cas (see Example 8), it is believed that FAK kinase function in the cochlea is playing a protective role in response to high level

20 noise exposure.

As described above, the PTK inhibitor treated ears showed less outer hair cell loss than controls. This indicates that anoikis (detachment from the cell's matrix, resulting in apoptosis) may play a significant role in noise-induced hair cell loss, and that blockage of apoptotic signals generated at the cell matrix can prevent hair cell

25 loss.

More specifically, using the above chinchilla animal model, it has been demonstrated that focal adhesion complexes are formed in response to extremely high level noise. FAK is activated upon formation of these complexes and is known to initiate several signaling cascades, first through a series of autophosphorylation events

30 and subsequently through phosphorylation of downstream peptide substrates. It has been demonstrated that apoptotic cells are seen within the lesion surrounded by focal adhesion complexes. Furthermore, addition of the pp60^{c-src} inhibitor prevents the

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apoptotic response without preventing the formation of the focal adhesion complex. These data suggest that the downstream signaling through tyrosine phosphorylation by FAK may be an early step in the apoptotic signaling of hair cells. Since FAK is activated by shear stress in other organic systems, these observations may represent
5 the first signaling pathway identified in the ear to be activated by mechanical stress.

Although preferred embodiments have been depicted and described in detail herein, it will be apparent to those skilled in the relevant art that various modifications, additions, substitutions, and the like can be made without departing from the spirit of the invention and these are therefore considered to be within the
10 scope of the invention as defined in the claims which follow.

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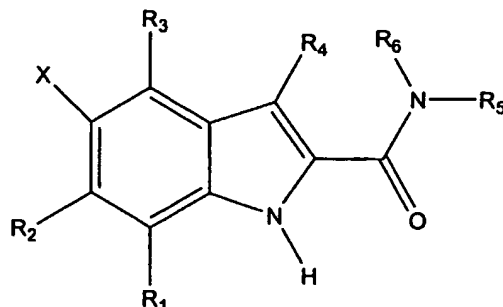
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What is claimed:

1. A non-peptide protein tyrosine kinase inhibitor or protein phosphatase inhibitor having the formula:



5

wherein X is a halogen;

- R_1 through R_6 may be the same or different, and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl;

- wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; or

- R_5 and R_6 together form a heterocyclic compound; and
wherein any of R_1 through R_6 and R_a through R_c is substituted or unsubstituted.

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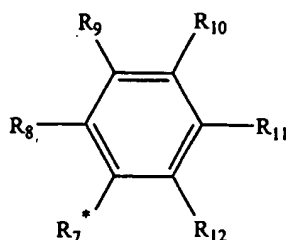
2. The non-peptide inhibitor according to claim 1, wherein at least one of R_5 or R_6 is

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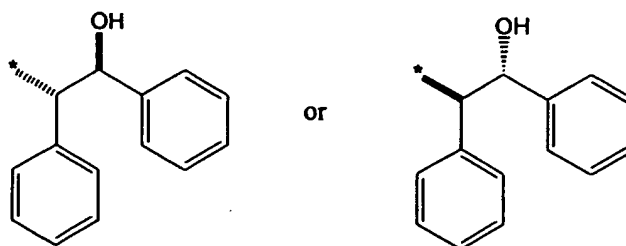


- wherein R_7^* is the point of attachment and is $(CH_2)_x$, wherein x is from 0 to 10, CH_2CHOH , $CH(CH_3)R$, or $CH(CH_3)S$, and each of R_8 through R_{12} may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; and

- wherein any of R_8 through R_{12} and R_a through R_c is substituted or unsubstituted.

3. The non-peptide inhibitor according to claim 1, wherein at least one of R_5 or R_6 is



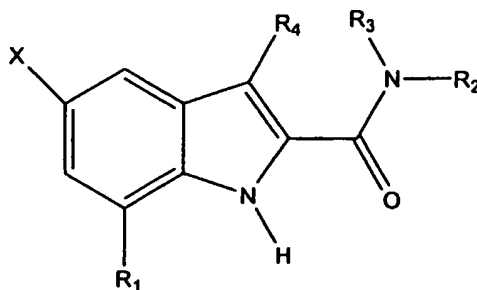
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wherein the asterisk indicates the point of attachment to the nitrogen.

4. The non-peptide inhibitor according to claim 1, wherein X is fluorine.
5. The non-peptide inhibitor according to claim 1, wherein the non-peptide inhibitor inhibits the activity of pp60^{c-src} tyrosine kinase.
6. The non-peptide inhibitor according to claim 1, wherein the non-peptide inhibitor inhibits the activity of protein tyrosine phosphatase 1B.
7. The non-peptide inhibitor according to claim 1, wherein the non-peptide inhibitor inhibits the activity of epidermal growth factor receptor tyrosine kinase.
8. The non-peptide inhibitor according to claim 1, wherein the non-peptide inhibitor inhibits the activity of p56 lck tyrosine kinase.
9. The non-peptide inhibitor according to claim 1, wherein the non-peptide inhibitor inhibits the activity of p55 fyn tyrosine kinase.
10. A non-peptide protein tyrosine kinase inhibitor or protein phosphatase inhibitor having the formula:

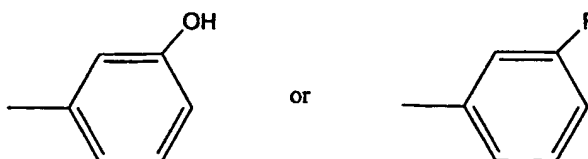


wherein X is a halogen, R₁ is H, R₂ is

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R₃ is H, and R₄ is H.

- 5 11. The non-peptide inhibitor according to claim 10, wherein X is fluorine.
12. The non-peptide inhibitor according to claim 10, wherein the non-peptide inhibitor inhibits the activity of pp60^{c-src} tyrosine kinase.
- 10 13. The non-peptide inhibitor according to claim 10, wherein the non-peptide inhibitor inhibits the activity of protein tyrosine phosphatase 1B.
14. The non-peptide inhibitor according to claim 10, wherein the non-peptide inhibitor inhibits the activity of epidermal growth factor receptor tyrosine
- 15 kinase.
15. The non-peptide inhibitor according to claim 10, wherein the non-peptide inhibitor inhibits the activity of p56 lck tyrosine kinase.
- 20 16. The non-peptide inhibitor according to claim 10, wherein the non-peptide inhibitor inhibits the activity of p55 fyn tyrosine kinase.
17. A method for identifying inhibitors of protein kinases comprising:
 providing at least one first module having one or more functional groups each
- 25 capable of covalently or non-covalently binding to catalytic residues of the protein kinase, wherein at least one of the one or more functional groups is a halogen;

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combining the at least one first module with at least one second module which provides a non-peptide scaffold to form one or more combinations of the first and second modules;

screening the one or more combinations of the first and second modules for protein kinase inhibition; and

selecting combinations of the first and second modules which inhibit protein kinase activity.

18. The method according to claim 17, wherein said providing at least one first module comprises:

attaching the at least one first module to a peptide scaffold;

identifying one or more functional groups on the first module which preferentially bind to catalytic residues of the protein kinase; and wherein said combining the at least one first module with the at least one second module

comprises:

substituting the at least one second module for the peptide scaffold.

19. The method according to claim 17, wherein the halogen is fluorine.

20. The method according to claim 17, wherein the at least one first module comprises two or more functional groups.

21. The method according to claim 20, wherein the at least one first module comprises a functional group selected from the group consisting of boronic acid, a hydroxyl group, phosphonic acid, sulfamic acid, a guanidino group, carboxylic acid, an aldehyde, an amide, and hydroxymethylphosphonic acid

22. The method according to claim 21, wherein the at least one first module comprises a boronic acid group.

23. The method according to claim 21, wherein the at least one first module comprises a hydroxyl group.

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24. The method according to claim 21, wherein the at least one first module comprises a amide group.
- 5 25. The method according to claim 24, wherein the amide group is a vicinal tricarbonyl amide.
26. The method according to claim 17, wherein the at least one second module is selected from the group consisting of indole, naphthalene, biphenyl,
10 isoquinoline, benzofuran, and benzothiophene.
27. The method according to claim 26, wherein the at least one second module comprises an indole.
- 15 28. The method according to claim 26, wherein the at least one second module comprises naphthalene.
29. The method according to claim 17, wherein the at least one first module further comprises a linear chain comprising between one and three carbon
20 atoms which links the at least one first module to at least one second module.
30. The method according to claim 29, wherein one of the carbon atoms in the linear chain is substituted with a nitrogen, oxygen, or sulfur atom.
- 25 31. The method according to claim 17, wherein the protein kinase is a protein tyrosine kinase.
32. The method according to claim 31, wherein the protein tyrosine kinase is selected from the group consisting of pp60^{c-src}, p56^{lck}, p55^{lyn}, ZAP kinase, platelet
30 derived growth factor receptor tyrosine kinase, Bcr-Abl, VEGF receptor tyrosine kinase, epidermal growth factor receptor tyrosine kinase, and epidermal growth factor receptor-like tyrosine kinases.

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33. The method according to claim 32, wherein the protein tyrosine kinase is pp60^{C-src}.

5 34. The method according to claim 17, wherein the protein kinase is a protein serine kinase.

35. The method according to claim 34, wherein the protein serine kinase is selected from the group consisting of MAP kinase, protein kinase C, and CDK kinase.

10

36. The method according to claim 17, further comprising:
attaching one or more specificity side chain elements to the one or more combinations of the first and second modules.

15 37. A method for identifying improved protein kinase inhibitors, comprising:
providing a first inhibitor produced according to the method of claim 17,
modifying the at least one first module, specificity side chain elements, or a combination thereof of the first inhibitor; and
20 identifying modified inhibitors which have an increased ability to inhibit protein kinase activity when compared to the unmodified first inhibitor.

38. The method according to claim 17, wherein the protein kinase inhibitor inhibits protein kinase activity but does not inhibit ATP binding to the protein kinase.

25

39. A method for testing compounds for an ability to inhibit protein kinase activity comprising:
providing a protein kinase inhibitor according to the method of claim 17,
measuring activity of the protein kinase in the presence of the inhibitor at a
30 same temperature, pH, ionic strength, osmolarity, and free magnesium concentration as found in a cell which expresses the protein kinase; and

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comparing the protein kinase activity to activity from the protein kinase
without the presence of the inhibitor.

40. A method of inhibiting a protein kinase comprising:
- 5 contacting the protein kinase with a compound comprising at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein kinase, wherein the one or more functional groups comprise a halogen, and a second module which provides a non-peptide scaffold, wherein the combination of the at least one first module and second
- 10 module inhibits the protein kinase's activity.
41. The method according to claim 40, wherein the halogen is fluorine.
42. The method according to claim 40, wherein the first module comprises
- 15 two or more functional groups.
43. The method according to claim 42, wherein the first module comprises a functional group selected from the group consisting of boronic acid, hydroxy, phosphonic acid, sulfamic acid, a guanidino group, carboxylic acid, an aldehyde, an
- 20 amide, and hydroxymethylphosphonic acid.
44. The method according to claim 43, wherein the first module comprises a boronic acid group.
- 25 45. The method according to claim 43, wherein the first module comprises a hydroxyl group.
46. The method according to claim 40, wherein the second module is selected from the group consisting of indole, naphthalene, biphenyl, isoquinoline,
- 30 benzofuran, and benzothiophene.

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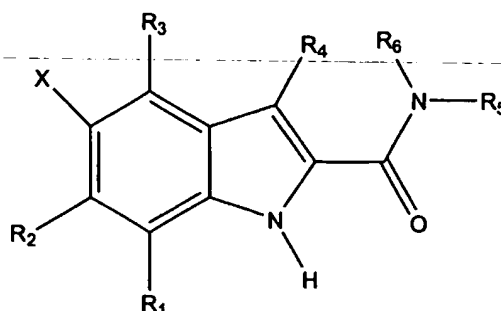
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47. The method according to claim 46, wherein the second module comprises an indole.
48. The method according to claim 46, wherein the second module comprises naphthalene.
49. The method according to claim 40, wherein a linear chain comprising between one and three carbon atoms links the first module to the second module.
50. The method according to claim 49, wherein one of the carbon atoms in the linear chain is substituted with a nitrogen, oxygen, or sulfur atom.
51. The method according to claim 40, wherein the protein kinase is a protein tyrosine kinase.
52. The method according to claim 51, wherein the protein tyrosine kinase is selected from the group consisting of pp60^{c-src}, p56^{lck}, p55^{lyn}, ZAP kinase, platelet derived growth factor receptor tyrosine kinase, Bcr-Abl, VEGF receptor tyrosine kinase, epidermal growth factor receptor tyrosine kinase and epidermal growth factor receptor-like tyrosine kinases.
53. The method according to claim 52, wherein the protein tyrosine kinase is pp60^{c-src}.
54. The method according to claim 53, wherein the compound has the following formula:

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wherein X is a halogen;

R_1 through R_6 may be the same or different, and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,

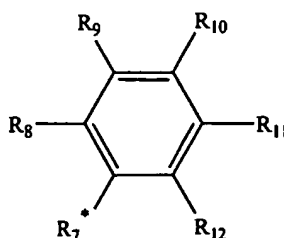
- 5 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl,
heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,
- 10 wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl, or

R_5 and R_6 together form a heterocyclic compound; and

wherein any of R_1 through R_6 and R_a through R_c is substituted or

- 15 unsubstituted.

55. The method according to claim 54, wherein at least one of R_5 or R_6 is



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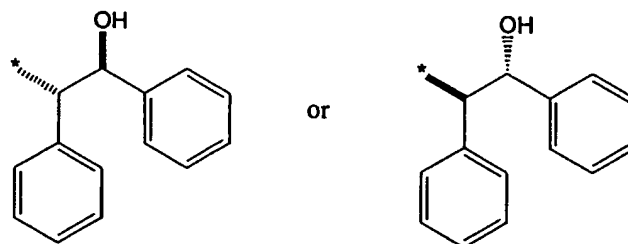
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- wherein R_7^* is the point of attachment and is $(CH_2)_x$, wherein X is from 0 to 10, CH_2CHOH , $CH(CH_3)R$, or $CH(CH_3)S$, and each of R_8 through R_{12} may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b ,
 5 $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,
 10 wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; and
 wherein any of R_8 through R_{12} and R_a through R_c is substituted or unsubstituted.

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56. The method according to claim 54, wherein at least one of R_5 or R_6 is



wherein the asterisk indicates the point of attachment to the nitrogen.

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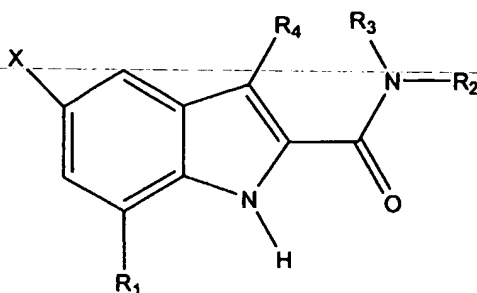
57. The method according to claim 54, wherein X is fluorine.

58. The method according to claim 53, wherein the compound has the following formula:

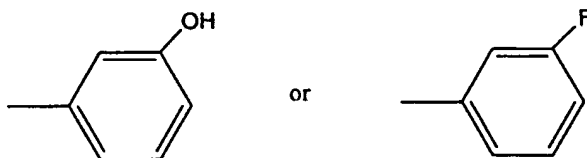
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wherein X is a halogen, R₁ is H, R₂ is



5 R₃ is H, and R₄ is H.

59. The method according to claim 58, wherein X is fluorine.

60. The method according to claim 40, wherein the protein kinase is a
10 protein serine kinase.

61. The method according to claim 60, wherein the protein serine kinase is selected from the group consisting of MAP kinase, protein kinase C, and CDK kinase.

15 62. The method according to claim 40, wherein the compound further comprises one or more specificity side chain elements attached to the combination of the at least one first module and second module.

63. A method of treating a condition, responsive to a protein kinase
20 inhibitor, in a subject comprising:

administering an effective dose of a protein kinase inhibitor to a subject wherein the protein kinase inhibitor comprises at least one first module having one or more functional groups each capable of covalently or non-covalently binding to

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catalytic residues of the protein kinase, wherein the one or more functional groups comprise a halogen, and a second module which provides a non-peptide scaffold, wherein the combination of the at least one first module and second module inhibits protein kinase activity.

5

64. The method according to claim 63, wherein the condition is selected from the group consisting of cancer, psoriasis, atherosclerosis, or immune system activity.

10

65. The method according to claim 63, wherein the halogen is fluorine.

66. The method according to claim 63, wherein the first module comprises two or more functional groups.

15

67. The method according to claim 66, wherein the first module comprises a functional group selected from the group consisting of boronic acid, hydroxy, phosphonic acid, sulfamic acid, a guanidino group, carboxylic acid, an aldehyde, an amide, and hydroxymethylphosphonic acid.

20

68. The method according to claim 67, wherein the first module comprises a boronic acid group.

69. The method according to claim 67, wherein the first module comprises a hydroxyl group.

25

70. The method according to claim 63, wherein the second module is selected from the group consisting of indole, naphthalene, biphenyl, isoquinoline, benzofuran, and benzothiophene.

30

71. The method according to claim 70, wherein the second module comprises indole.

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72. The method according to claim 70, wherein the second module
comprises naphthalene.

73. The method according to claim 63, wherein a linear chain comprising
5 between one and three carbon atoms links the at least one first module to the second
module.

74. The method according to claim 73, wherein one of the carbon atoms in
the linear chain is substituted with a nitrogen, oxygen, or sulfur atom.

10

75. The method according to claim 63, wherein the protein kinase is a
protein tyrosine kinase.

76. The method according to claim 75, wherein the protein tyrosine kinase
15 is selected from the group consisting of pp60^{c-src}, p56^{lck}, p55^{lyn}, ZAP kinase, platelet
derived growth factor receptor tyrosine kinase, Bcr-Abl, VEGF receptor tyrosine
kinase, epidermal growth factor receptor tyrosine kinase, and epidermal growth factor
receptor-like tyrosine kinases.

20 77. The method according to claim 76, wherein the protein tyrosine kinase
is pp60^{c-src}.

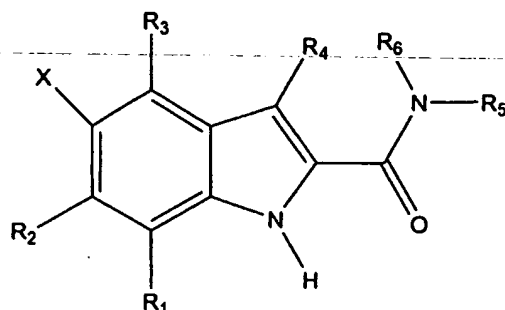
78. The method according to claim 77, wherein the compound has the
following formula:

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wherein X is a halogen;

R₁ through R₆ may be the same or different, and are selected from the group consisting of H, C(O)R_a, C(O)NR_aR_b, C(O)OR_a, C(O)SR_a, OH, OR_a, OC(O)R_a,

5 OC(O)OR_a, NH₂, NR_aR_b, NR_aC(O)R_b, NR_aC(O)NR_bR_c, NR_aC(O)OR_b, NR_aC(O)SR_b,
NR_aS(O)R_b, NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b, NR_aP(O)OR_bOR_c,
NR_aP(O)OR_bR_c, NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a, S(O)OR_a, S(O)₂OR_a,
S(O)NR_aR_b, S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl, heteroaryl, biaryl,
heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,

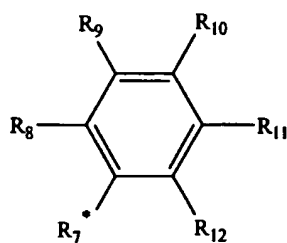
10 wherein R_a, R_b, and R_c may be the same or different and are selected
from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched,
cyclic, or unbranched alkyl, or

R₅ and R₆ together form a heterocyclic compound; and

wherein any of R₁ through R₆ and R_a through R_c is substituted or

15 unsubstituted.

79. The method according to claim 78, wherein at least one of R₅ or R₆ is



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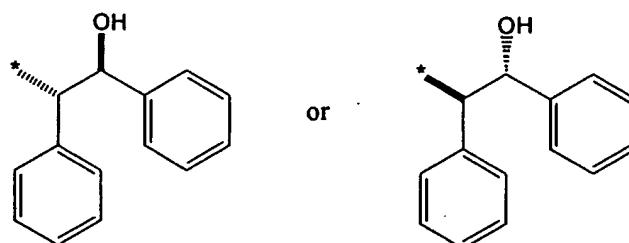
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- wherein R_7^* is the point of attachment and is $(CH_2)_x$, wherein X is from 0 to 10, CH_2CHOH , $CH(CH_3)R_7$, or $CH(CH_3)S_7$, and each of R_8 through R_{12} may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,
- wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; and
- wherein any of R_8 through R_{12} and R_a through R_c is substituted or unsubstituted.

15

80. The method according to claim 78, wherein at least one of R_5 or R_6 is



wherein the asterisk indicates the point of attachment to the nitrogen.

20

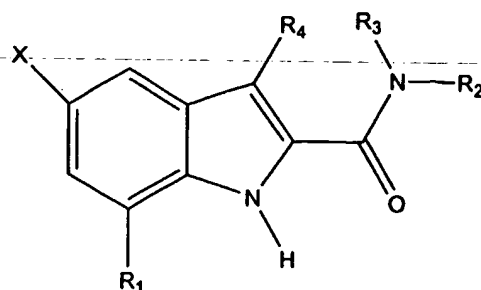
81. The method according to claim 78, wherein X is fluorine.

82. The method according to claim 77, wherein the compound has the following formula:

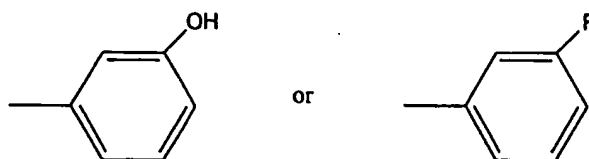
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wherein X is a halogen, R₁ is H, R₂ is



R₃ is H, and R₄ is H.

5

83. The method according to claim 82, wherein X is fluorine.

84. The method according to claim 63, wherein the protein kinase is a protein serine kinase.

10

85. The method according to claim 84, wherein the protein serine kinase is selected from the group consisting of MAP kinase, protein kinase C, and CDK kinase.

86. The method according to claim 63, wherein the compound further comprises one or more specificity side chain elements attached to the combination of the at least one first module and second module.

15

87. A method for identifying inhibitors of protein phosphatases comprising:

20 providing at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein phosphatase;

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combining the at least one first module with at least one second module which provides a non-peptide scaffold to form one or more combinations of the first and second modules;

5 screening the one or more combinations of the first and second modules for protein phosphatase inhibition; and

selecting combinations of the first and second modules which inhibit protein phosphatase activity.

88. The method according to claim 87, wherein said providing at least one
10 first module comprises:

attaching the at least one first module to a peptide scaffold;

identifying one or more functional groups on the first module which preferentially bind to catalytic residues of the protein phosphatase; and

wherein said combining the at least one first module with the at least one
15 second module comprises:

substituting the at least one second module for the peptide scaffold.

89. The method according to claim 87, wherein the at least one first
20 module comprises two or more functional groups.

90. The method according to claim 87, wherein the at least one first
module comprises a functional group selected from the group consisting of a halogen,
boronic acid, a hydroxyl group, phosphonic acid, sulfamic acid, a guanidino group,
carboxylic acid, an aldehyde, an amide, and hydroxymethylphosphonic acid

25

91. The method according to claim 90, wherein the at least one first
module comprises a halogen.

92. The method according to claim 90, wherein the at least one first
30 module comprises a boronic acid group.

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93. The method according to claim 90, wherein the at least one first module comprises a hydroxyl group.

94. The method according to claim 90, wherein the at least one first
5 module comprises an amide group.

95. The method according to claim 94, wherein the amide group is a vicinal tricarbonyl amide.

10 96. The method according to claim 87, wherein the at least one second module is selected from the group consisting of indole, naphthalene, biphenyl, isoquinoline, benzofuran, and benzothiophene.

97. The method according to claim 96, wherein the at least one second
15 module comprises an indole.

98. The method according to claim 96, wherein the at least one second module comprises naphthalene.

20 99. The method according to claim 87, wherein the at least one first module further comprises a linear chain comprising between one and three carbon atoms which links the at least one first module to at least one second module.

100. The method according to claim 99, wherein one of the carbon atoms in
25 the linear chain is substituted with a nitrogen, oxygen, or sulfur atom.

101. The method according to claim 87, wherein the protein phosphatase is protein tyrosine phosphatase 1B.

30 102. The method according to claim 87, further comprising:
attaching one or more specificity side chain elements to the one or more combinations of the first and second modules.

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103. A method for identifying improved protein phosphatase inhibitors, comprising:

providing a first inhibitor produced according to the method of claim 87,
5 modifying the at least one first module, specificity side chain elements, or a combination thereof of the first inhibitor; and
identifying modified inhibitors which have an increased ability to inhibit protein phosphatase activity when compared to the unmodified first inhibitor.

10 104. A method for testing compounds for an ability to inhibit protein phosphatase activity comprising:

providing a protein phosphatase inhibitor according to the method of claim 87,
measuring activity of the protein phosphatase in the presence of the inhibitor
at a same temperature, pH, ionic strength, osmolarity, and free magnesium
15 concentration as found in a cell which expresses the protein phosphatase; and
comparing the protein phosphatase activity to activity from the protein phosphatase without the presence of the inhibitor.

105. A method of inhibiting a protein phosphatase comprising:

20 contacting the protein phosphatase with a compound comprising at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein phosphatase, and a second module which provides a non-peptide scaffold, wherein the combination of the at least one first module and second module inhibits the protein phosphatase's activity.

25 106. The method according to claim 105, wherein the first module comprises two or more functional groups.

107. The method according to claim 105, wherein the first module
30 comprises a functional group selected from the group consisting of a halogen, boronic acid, hydroxy, phosphonic acid, sulfamic acid, a guanidino group, carboxylic acid, an aldehyde, an amide, and hydroxymethylphosphonic acid.

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108. The method according to claim 107, wherein the first module comprises a halogen.

5 109. The method according to claim 107, wherein the first module comprises a boronic acid group.

110. The method according to claim 107, wherein the first module comprises a hydroxyl group.

10

111. The method according to claim 105, wherein the second module is selected from the group consisting of indole, naphthalene, biphenyl, isoquinoline, benzofuran, and benzothiophene.

15 112. The method according to claim 111, wherein the second module comprises an indole.

113. The method according to claim 111, wherein the second module comprises naphthalene.

20

114. The method according to claim 105, wherein a linear chain comprising between one and three carbon atoms links the at least one first module to the second module.

25 115. The method according to claim 114, wherein one of the carbon atoms in the linear chain is substituted with a nitrogen, oxygen, or sulfur atom.

116. The method according to claim 105, wherein the protein phosphatase is protein tyrosine phosphatase 1B.

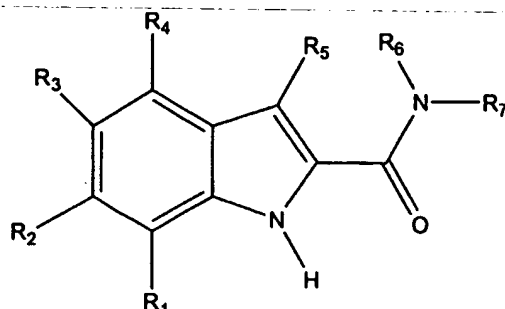
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117. The method according to claim 105, wherein the compound has the following formula:

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wherein R_1 through R_7 may be the same or different, and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 5 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl,
 heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,
 10 wherein R_a , R_b , and R_c may be the same or different and are selected
 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched,
 cyclic, or unbranched alkyl, or

R_6 and R_7 together form a heterocyclic compound; and

15 wherein any of R_1 through R_7 and R_a through R_c is substituted or
 unsubstituted.

118. The method according to claim 117, wherein R_3 is a halogen.

119. The method according to claim 118, wherein R_3 is fluorine.

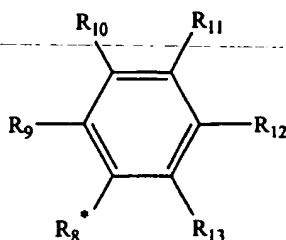
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120. The method according to claim 117, wherein at least one of R_6 or R_7 is

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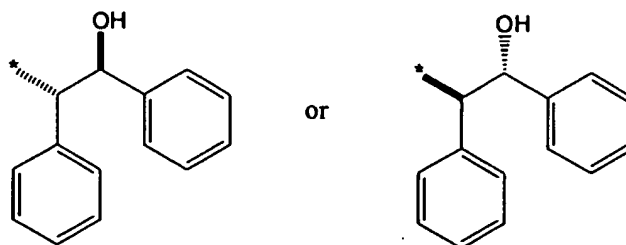
wherein R_8^* is the point of attachment and is $(CH_2)_x$, wherein X is from 0 to 10, CH_2CHOH , $CH(CH_3)R$, or $CH(CH_3)S$, and each of R_9 through R_{13} may be the same or different and are selected from the group consisting of H, $C(O)R_a$,

- 5 $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and a
- 10 branched, cyclic, or unbranched alkyl,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; and

- wherein any of R_9 through R_{13} and R_a through R_c is substituted or
- 15 unsubstituted.

121. The method according to claim 117, wherein at least one of R_6 or R_7 is



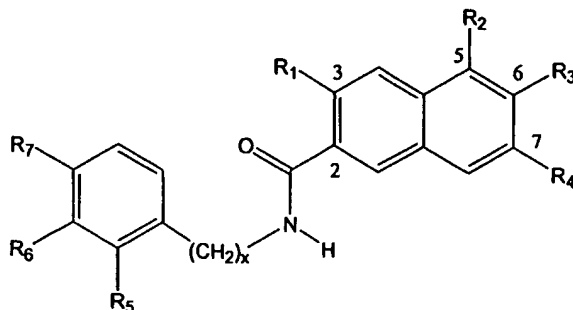
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wherein the asterisk indicates the point of attachment to the nitrogen.

122. The method according to claim 105, wherein the compound has the formula



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wherein each of R_1 through R_7 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,

15 wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; and

wherein any of R_1 through R_7 and R_a through R_c is substituted or unsubstituted; and

20 X is 0 or 1.

123. The method according to claim 105, wherein the compound further comprises one or more specificity side chain elements attached to the combination of the at least one first module and second module.

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124. A method of treating a condition, responsive to a protein phosphatase inhibitor, in a subject comprising:

administering an effective dose of a protein phosphatase inhibitor to a subject wherein the protein phosphatase inhibitor comprises at least one first module having one or more functional groups each capable of covalently or non-covalently binding to catalytic residues of the protein phosphatase, and a second module which provides a non-peptide scaffold, wherein the combination of the at least one first module and second module inhibits protein phosphatase activity.

125. The method according to claim 124, wherein the condition is selected from the group consisting of cancer, Type II diabetes, and obesity.

126. The method according to claim 124, wherein the first module comprises two or more functional groups.

127. The method according to claim 124, wherein the first module comprises a functional group selected from the group consisting of boronic acid, hydroxy, phosphonic acid, sulfamic acid, a guanidino group, carboxylic acid, an aldehyde, an amide, and hydroxymethylphosphonic acid.

128. The method according to claim 127, wherein the first module comprises a halogen.

129. The method according to claim 127, wherein the first module comprises a boronic acid group.

130. The method according to claim 127, wherein the first module comprises a hydroxyl group.

131. The method according to claim 124, wherein the second module is selected from the group consisting of indole, naphthalene, biphenyl, isoquinoline, benzofuran, and benzothiophene.

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132. The method according to claim 131, wherein the second module comprises indole.

5 133. The method according to claim 131, wherein the second module comprises naphthalene.

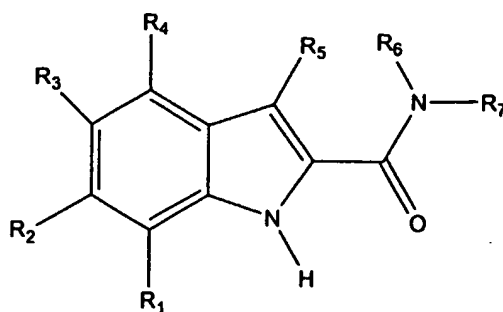
134. The method according to claim 124, wherein a linear chain comprising between one and three carbon atoms links the at least one first module to the second
10 module.

135. The method according to claim 134, wherein one of the carbon atoms in the linear chain is substituted with a nitrogen, oxygen, or sulfur atom.

15 136. The method according to claim 124, wherein the protein phosphatase is protein tyrosine phosphatase 1B.

137. The method according to claim 124, wherein the compound has the following formula:

20



wherein R_1 through R_7 may be the same or different, and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
25 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,

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$S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,

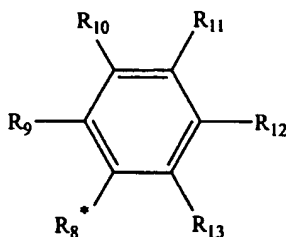
wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl, or

R_6 and R_7 together form a heterocyclic compound; and wherein any of R_1 through R_7 and R_a through R_c is substituted or unsubstituted.

138. The method according to claim 137, wherein R_3 is a halogen.

139. The method according to claim 138, wherein R_3 is fluorine.

140. The method according to claim 137, wherein at least one of R_6 or R_7 is



wherein R_8^* is the point of attachment and is $(CH_2)_x$, wherein X is from 0 to 10, CH_2CHOH , $CH(CH_3)R$, or $CH(CH_3)S$, and each of R_9 through R_{13} may be the same or different and are selected from the group consisting of H, $C(O)R_a$,

$C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,

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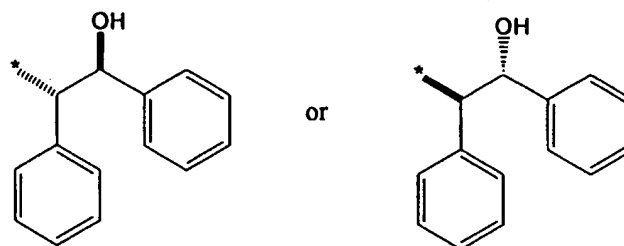
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wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; and

wherein any of R_9 through R_{13} and R_a through R_c is substituted or
5 unsubstituted.

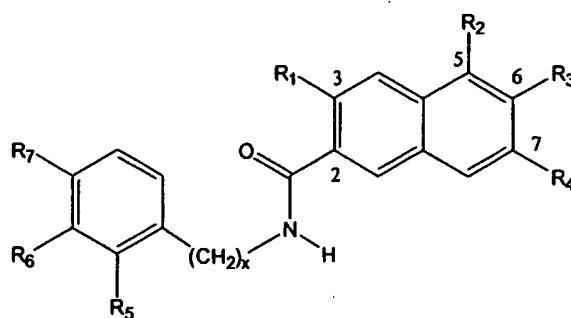
141. The method according to claim 137, wherein at least one of R_6 or R_7 is



wherein the asterisk indicates the point of attachment to the nitrogen.

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142. The method according to claim 124, wherein the compound has the formula:



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wherein each of R_1 through R_7 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$,

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$S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and a branched, cyclic, or unbranched alkyl,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; and

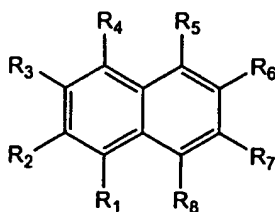
wherein any of R_1 through R_7 and R_a through R_c is substituted or unsubstituted; and

X is 0 or 1.

10

143. The method according to claim 124, wherein the compound further comprises one or more specificity side chain elements attached to the combination of the at least one first module and second module.

144. The method according to claim 40, wherein the compound has the following formula:



wherein R_1 through R_8 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

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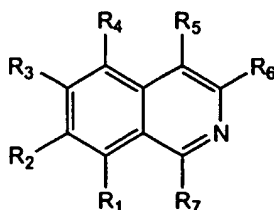
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wherein any of R_1 through R_8 and R_a through R_c may be substituted or unsubstituted; provided that at least one of R_1 through R_8 is a halogen.

145. The method according to claim 40, wherein the compound has the following formula:

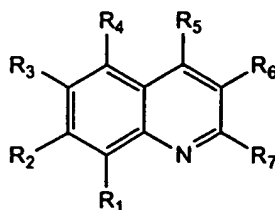


wherein R_1 through R_7 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_7 and R_a through R_c may be substituted or unsubstituted.

146. The method according to claim 40, wherein the compound has the following formula:



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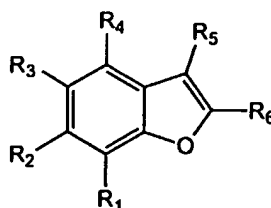
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wherein R_1 through R_7 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 5 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected
 10 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_7 and R_a through R_c may be substituted or unsubstituted.

15 147. The method according to claim 40, wherein the compound has the following formula:



20 wherein R_1 through R_6 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 25 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

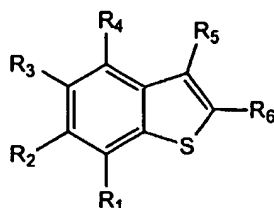
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wherein any of R_1 through R_6 and R_a through R_c may be substituted or unsubstituted.

148. The method according to claim 40, wherein the compound has the
5 following formula:

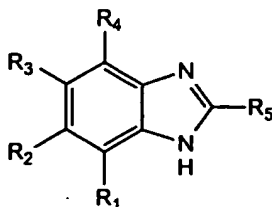


wherein R_1 through R_6 may be the same or different and are selected from the
10 group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
15 a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected
from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_6 and R_a through R_c may be substituted or
20 unsubstituted.

149. The method according to claim 40, wherein the compound has the
following formula:



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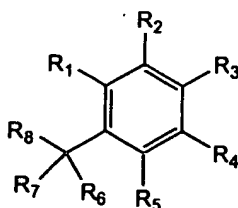
wherein R_1 through R_5 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 5 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

10 wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_5 and R_a through R_c may be substituted or unsubstituted.

15

150. The method according to claim 40, wherein the compound has the following formula:



20

wherein R_1 through R_8 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 25 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

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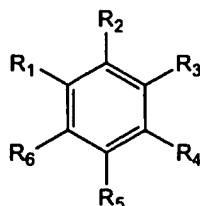
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wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_6 and R_a through R_c may be substituted or
 5 unsubstituted.

151. The method according to claim 40, wherein the compound has the following formula:

10



wherein R_1 through R_6 may be the same or different and are selected from the
 15 group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
 20 a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

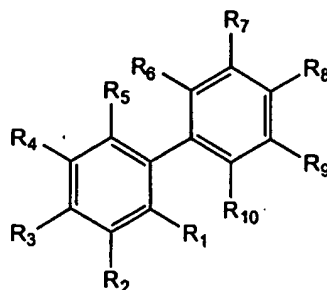
wherein any of R_1 through R_6 and R_a through R_c may be substituted or
 25 unsubstituted.

152. The method according to claim 40, wherein the compound has the following formula:

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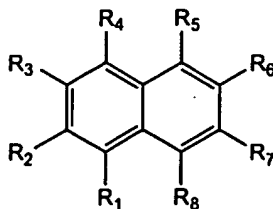
wherein R_1 through R_{10} may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 5 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

10 wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_{10} and R_a through R_c may be substituted or unsubstituted.

15

153. The method according to claim 63, wherein the compound has the following formula:



20

wherein R_1 through R_8 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,

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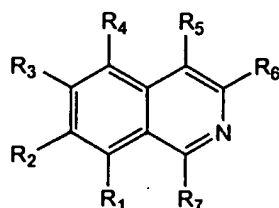
NR_aS(O)R_b, NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b, NR_aP(O)OR_bOR_c,
 NR_aP(O)OR_bR_c, NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a, S(O)OR_a, S(O)₂OR_a,
 S(O)NR_aR_b, S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

5 wherein R_a, R_b, and R_c may be the same or different and are selected
 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 cyclic, or unbranched alkyl group; and

 wherein any of R₁ through R₈ and R_a through R_c may be substituted or
 unsubstituted; provided that at least one of R₁ through R₈ is a halogen.

10

154. The method according to claim 63, wherein the compound has the
 following formula:



15

 wherein R₁ through R₇ may be the same or different and are selected from the
 group consisting of H, C(O)R_a, C(O)NR_aR_b, C(O)OR_a, C(O)SR_a, OH, OR_a, OC(O)R_a,
 OC(O)OR_a, NH₂, NR_aR_b, NR_aC(O)R_b, NR_aC(O)NR_bR_c, NR_aC(O)OR_b, NR_aC(O)SR_b,
 NR_aS(O)R_b, NR_aS(O)₂R_b, NR_aS(O)OR_b, NR_aS(O)₂OR_b, NR_aP(O)OR_bOR_c,
 20 NR_aP(O)OR_bR_c, NR_aP(O)OR_bOR_c, SR_a, S(O)R_a, S(O)₂R_a, S(O)OR_a, S(O)₂OR_a,
 S(O)NR_aR_b, S(O)₂NR_aR_b, P(O)OR_aOR_b, B(OH)₂, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

 wherein R_a, R_b, and R_c may be the same or different and are selected
 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 25 cyclic, or unbranched alkyl group; and

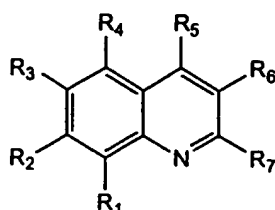
 wherein any of R₁ through R₇ and R_a through R_c may be substituted or
 unsubstituted.

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155. The method according to claim 63, wherein the compound has the following formula:



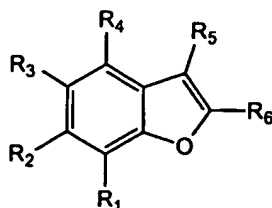
5

wherein R_1 through R_7 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 10 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 15 cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_7 and R_a through R_c may be substituted or unsubstituted.

156. The method according to claim 63, wherein the compound has the
 20 following formula:



wherein R_1 through R_6 may be the same or different and are selected from the
 25 group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,

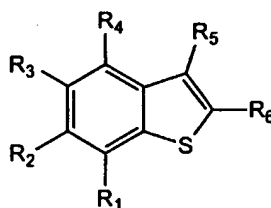
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- OC(O)OR_a , NH_2 , NR_aR_b , $\text{NR}_a\text{C(O)R}_b$, $\text{NR}_a\text{C(O)NR}_b\text{R}_c$, $\text{NR}_a\text{C(O)OR}_b$, $\text{NR}_a\text{C(O)SR}_b$,
 $\text{NR}_a\text{S(O)R}_b$, $\text{NR}_a\text{S(O)}_2\text{R}_b$, $\text{NR}_a\text{S(O)OR}_b$, $\text{NR}_a\text{S(O)}_2\text{OR}_b$, $\text{NR}_a\text{P(O)OR}_b\text{OR}_c$,
 $\text{NR}_a\text{P(O)OR}_b\text{R}_c$, $\text{NR}_a\text{P(O)OR}_b\text{OR}_c$, SR_a , S(O)R_a , $\text{S(O)}_2\text{R}_a$, S(O)OR_a , $\text{S(O)}_2\text{OR}_a$,
 $\text{S(O)NR}_a\text{R}_b$, $\text{S(O)}_2\text{NR}_a\text{R}_b$, $\text{P(O)OR}_a\text{OR}_b$, B(OH)_2 , halogen, aryl, heteroaryl, biaryl, and
 5 a branched, cyclic, or unbranched alkyl group,
 wherein R_a , R_b , and R_c may be the same or different and are selected
 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 cyclic, or unbranched alkyl group; and
 wherein any of R_1 through R_6 and R_a through R_c may be substituted or
 10 unsubstituted.

157. The method according to claim 63, wherein the compound has the following formula:



15

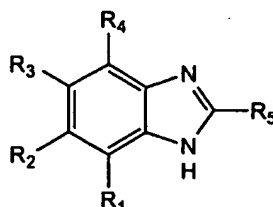
- wherein R_1 through R_6 may be the same or different and are selected from the
 group consisting of H, C(O)R_a , $\text{C(O)NR}_a\text{R}_b$, C(O)OR_a , C(O)SR_a , OH, OR_a , OC(O)R_a ,
 OC(O)OR_a , NH_2 , NR_aR_b , $\text{NR}_a\text{C(O)R}_b$, $\text{NR}_a\text{C(O)NR}_b\text{R}_c$, $\text{NR}_a\text{C(O)OR}_b$, $\text{NR}_a\text{C(O)SR}_b$,
 20 $\text{NR}_a\text{S(O)R}_b$, $\text{NR}_a\text{S(O)}_2\text{R}_b$, $\text{NR}_a\text{S(O)OR}_b$, $\text{NR}_a\text{S(O)}_2\text{OR}_b$, $\text{NR}_a\text{P(O)OR}_b\text{OR}_c$,
 $\text{NR}_a\text{P(O)OR}_b\text{R}_c$, $\text{NR}_a\text{P(O)OR}_b\text{OR}_c$, SR_a , S(O)R_a , $\text{S(O)}_2\text{R}_a$, S(O)OR_a , $\text{S(O)}_2\text{OR}_a$,
 $\text{S(O)NR}_a\text{R}_b$, $\text{S(O)}_2\text{NR}_a\text{R}_b$, $\text{P(O)OR}_a\text{OR}_b$, B(OH)_2 , halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,
 wherein R_a , R_b , and R_c may be the same or different and are selected
 25 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 cyclic, or unbranched alkyl group; and
 wherein any of R_1 through R_6 and R_a through R_c may be substituted or
 unsubstituted.

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158. The method according to claim 63, wherein the compound has the following formula:



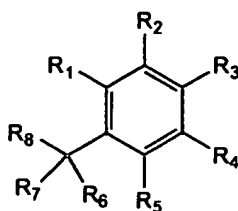
5

wherein R_1 through R_5 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 10 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected
 15 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_5 and R_a through R_c may be substituted or
 unsubstituted.

20 159. The method according to claim 63, wherein the compound has the following formula:



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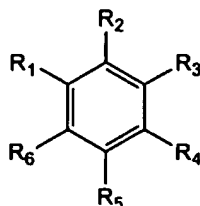
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- wherein R_1 through R_8 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 5 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

- wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 10 cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_8 and R_a through R_c may be substituted or unsubstituted.

160. The method according to claim 63, wherein the compound has the
 15 following formula:



20

- wherein R_1 through R_6 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 25 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

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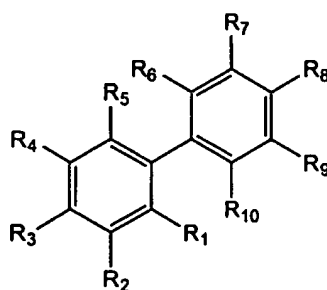
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wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_6 and R_a through R_c may be substituted or
 5 unsubstituted.

161. The method according to claim 63, wherein the compound has the following formula:



10

wherein R_1 through R_{10} may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 15 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected
 20 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

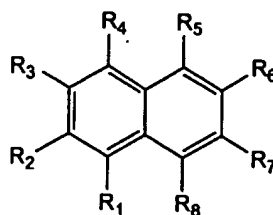
wherein any of R_1 through R_{10} and R_a through R_c may be substituted or unsubstituted.

25 162. The method according to claim 105, wherein the compound has the following formula:

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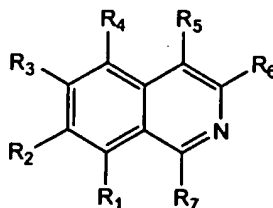
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- wherein R_1 through R_8 may be the same or different and are selected from the
- 5 group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
- 10 a branched, cyclic, or unbranched alkyl group,
- wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and
- wherein any of R_1 through R_8 and R_a through R_c may be substituted or
- 15 unsubstituted; provided that at least one of R_1 through R_8 is a halogen.

163. The method according to claim 105, wherein the compound has the following formula:



20

- wherein R_1 through R_7 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
- 25 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,

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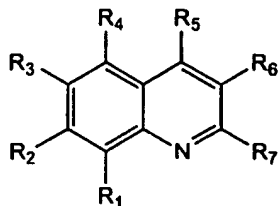
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$\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{R}_c$, $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{OR}_c$, SR_a , $\text{S}(\text{O})\text{R}_a$, $\text{S}(\text{O})_2\text{R}_a$, $\text{S}(\text{O})\text{OR}_a$, $\text{S}(\text{O})_2\text{OR}_a$,
 $\text{S}(\text{O})\text{NR}_a\text{R}_b$, $\text{S}(\text{O})_2\text{NR}_a\text{R}_b$, $\text{P}(\text{O})\text{OR}_a\text{OR}_b$, $\text{B}(\text{OH})_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected
 5 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_7 and R_a through R_c may be substituted or
 unsubstituted.

10 164. The method according to claim 105, wherein the compound has the
 following formula:



15 wherein R_1 through R_7 may be the same or different and are selected from the
 group consisting of H, $\text{C}(\text{O})\text{R}_a$, $\text{C}(\text{O})\text{NR}_a\text{R}_b$, $\text{C}(\text{O})\text{OR}_a$, $\text{C}(\text{O})\text{SR}_a$, OH, OR_a , $\text{OC}(\text{O})\text{R}_a$,
 $\text{OC}(\text{O})\text{OR}_a$, NH_2 , NR_aR_b , $\text{NR}_a\text{C}(\text{O})\text{R}_b$, $\text{NR}_a\text{C}(\text{O})\text{NR}_b\text{R}_c$, $\text{NR}_a\text{C}(\text{O})\text{OR}_b$, $\text{NR}_a\text{C}(\text{O})\text{SR}_b$,
 $\text{NR}_a\text{S}(\text{O})\text{R}_b$, $\text{NR}_a\text{S}(\text{O})_2\text{R}_b$, $\text{NR}_a\text{S}(\text{O})\text{OR}_b$, $\text{NR}_a\text{S}(\text{O})_2\text{OR}_b$, $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{OR}_c$,
 $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{R}_c$, $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{OR}_c$, SR_a , $\text{S}(\text{O})\text{R}_a$, $\text{S}(\text{O})_2\text{R}_a$, $\text{S}(\text{O})\text{OR}_a$, $\text{S}(\text{O})_2\text{OR}_a$,
 20 $\text{S}(\text{O})\text{NR}_a\text{R}_b$, $\text{S}(\text{O})_2\text{NR}_a\text{R}_b$, $\text{P}(\text{O})\text{OR}_a\text{OR}_b$, $\text{B}(\text{OH})_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected
 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 cyclic, or unbranched alkyl group; and

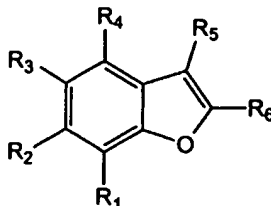
25 wherein any of R_1 through R_7 and R_a through R_c may be substituted or
 unsubstituted.

165. The method according to claim 105, wherein the compound has the
 following formula:

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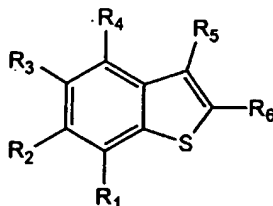


- wherein R_1 through R_6 may be the same or different and are selected from the
- 5 group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
- 10 a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

- wherein any of R_1 through R_6 and R_a through R_c may be substituted or
- 15 unsubstituted.

166. The method according to claim 105, wherein the compound has the following formula:



20

- wherein R_1 through R_6 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
- 25 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,

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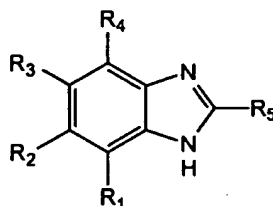
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$\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{R}_c$, $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{OR}_c$, SR_a , $\text{S}(\text{O})\text{R}_a$, $\text{S}(\text{O})_2\text{R}_a$, $\text{S}(\text{O})\text{OR}_a$, $\text{S}(\text{O})_2\text{OR}_a$,
 $\text{S}(\text{O})\text{NR}_a\text{R}_b$, $\text{S}(\text{O})_2\text{NR}_a\text{R}_b$, $\text{P}(\text{O})\text{OR}_a\text{OR}_b$, $\text{B}(\text{OH})_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

- wherein R_a , R_b , and R_c may be the same or different and are selected
 5 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 cyclic, or unbranched alkyl group; and
 wherein any of R_1 through R_6 and R_a through R_c may be substituted or
 unsubstituted.

- 10 167. The method according to claim 105, wherein the compound has the
 following formula:



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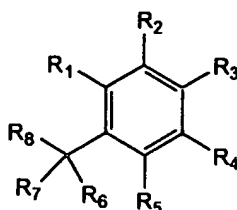
- wherein R_1 through R_5 may be the same or different and are selected from the
 group consisting of H, $\text{C}(\text{O})\text{R}_a$, $\text{C}(\text{O})\text{NR}_a\text{R}_b$, $\text{C}(\text{O})\text{OR}_a$, $\text{C}(\text{O})\text{SR}_a$, OH, OR_a , $\text{OC}(\text{O})\text{R}_a$,
 $\text{OC}(\text{O})\text{OR}_a$, NH_2 , NR_aR_b , $\text{NR}_a\text{C}(\text{O})\text{R}_b$, $\text{NR}_a\text{C}(\text{O})\text{NR}_b\text{R}_c$, $\text{NR}_a\text{C}(\text{O})\text{OR}_b$, $\text{NR}_a\text{C}(\text{O})\text{SR}_b$,
 $\text{NR}_a\text{S}(\text{O})\text{R}_b$, $\text{NR}_a\text{S}(\text{O})_2\text{R}_b$, $\text{NR}_a\text{S}(\text{O})\text{OR}_b$, $\text{NR}_a\text{S}(\text{O})_2\text{OR}_b$, $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{OR}_c$,
 20 $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{R}_c$, $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{OR}_c$, SR_a , $\text{S}(\text{O})\text{R}_a$, $\text{S}(\text{O})_2\text{R}_a$, $\text{S}(\text{O})\text{OR}_a$, $\text{S}(\text{O})_2\text{OR}_a$,
 $\text{S}(\text{O})\text{NR}_a\text{R}_b$, $\text{S}(\text{O})_2\text{NR}_a\text{R}_b$, $\text{P}(\text{O})\text{OR}_a\text{OR}_b$, $\text{B}(\text{OH})_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,
 wherein R_a , R_b , and R_c may be the same or different and are selected
 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 25 cyclic, or unbranched alkyl group; and
 wherein any of R_1 through R_5 and R_a through R_c may be substituted or
 unsubstituted.

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168. The method according to claim 105, wherein the compound has the following formula:



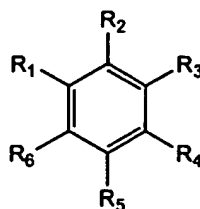
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wherein R_1 through R_8 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

10 wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

15 wherein any of R_1 through R_8 and R_a through R_c may be substituted or unsubstituted.

169. The method according to claim 105, wherein the compound has the following formula:



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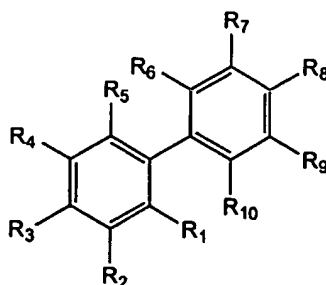
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wherein R_1 through R_6 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 5 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 10 cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_6 and R_a through R_c may be substituted or unsubstituted.

170. The method according to claim 105, wherein the compound has the
 15 following formula:



wherein R_1 through R_{10} may be the same or different and are selected from the
 20 group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
 25 a branched, cyclic, or unbranched alkyl group,

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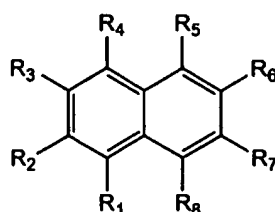
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wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_{10} and R_a through R_c may be substituted or
 5 unsubstituted.

171. The method according to claim 124, wherein the compound has the following formula:



10

wherein R_1 through R_8 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 15 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected
 20 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

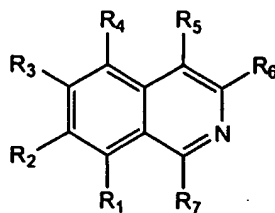
wherein any of R_1 through R_8 and R_a through R_c may be substituted or unsubstituted; provided that at least one of R_1 through R_8 is a halogen.

25 172. The method according to claim 124, wherein the compound has the following formula:

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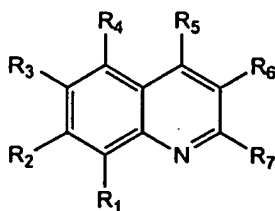
wherein R_1 through R_7 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 5 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

10 wherein R_a , R_b , and R_c may be the same or different and are selected
 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_7 and R_a through R_c may be substituted or
 unsubstituted.

15

173. The method according to claim 124, wherein the compound has the
 following formula:



20

wherein R_1 through R_7 may be the same or different and are selected from the
 group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 25 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,

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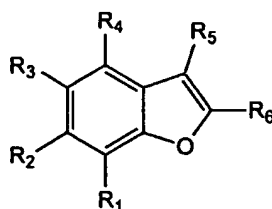
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$S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_7 and R_a through R_c may be substituted or unsubstituted.

174. The method according to claim 124, wherein the compound has the following formula:



wherein R_1 through R_6 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

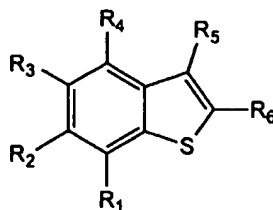
wherein any of R_1 through R_6 and R_a through R_c may be substituted or unsubstituted.

175. The method according to claim 124, wherein the compound has the following formula:

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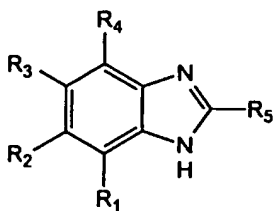
wherein R_1 through R_6 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 5 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$,
 $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

10 wherein R_a , R_b , and R_c may be the same or different and are selected
 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_6 and R_a through R_c may be substituted or
 unsubstituted.

15

176. The method according to claim 124, wherein the compound has the
 following formula:



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wherein R_1 through R_5 may be the same or different and are selected from the
 group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$,
 $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 25 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,

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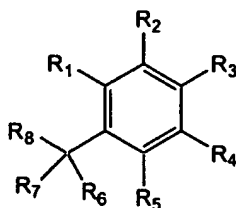
$\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{R}_c$, $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{OR}_c$, SR_a , $\text{S}(\text{O})\text{R}_a$, $\text{S}(\text{O})_2\text{R}_a$, $\text{S}(\text{O})\text{OR}_a$, $\text{S}(\text{O})_2\text{OR}_a$,
 $\text{S}(\text{O})\text{NR}_a\text{R}_b$, $\text{S}(\text{O})_2\text{NR}_a\text{R}_b$, $\text{P}(\text{O})\text{OR}_a\text{OR}_b$, $\text{B}(\text{OH})_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected

- 5 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_5 and R_a through R_c may be substituted or unsubstituted.

- 10 177. The method according to claim 124, wherein the compound has the following formula:



- 15 wherein R_1 through R_8 may be the same or different and are selected from the group consisting of H, $\text{C}(\text{O})\text{R}_a$, $\text{C}(\text{O})\text{NR}_a\text{R}_b$, $\text{C}(\text{O})\text{OR}_a$, $\text{C}(\text{O})\text{SR}_a$, OH, OR_a , $\text{OC}(\text{O})\text{R}_a$, $\text{OC}(\text{O})\text{OR}_a$, NH_2 , NR_aR_b , $\text{NR}_a\text{C}(\text{O})\text{R}_b$, $\text{NR}_a\text{C}(\text{O})\text{NR}_b\text{R}_c$, $\text{NR}_a\text{C}(\text{O})\text{OR}_b$, $\text{NR}_a\text{C}(\text{O})\text{SR}_b$,
 $\text{NR}_a\text{S}(\text{O})\text{R}_b$, $\text{NR}_a\text{S}(\text{O})_2\text{R}_b$, $\text{NR}_a\text{S}(\text{O})\text{OR}_b$, $\text{NR}_a\text{S}(\text{O})_2\text{OR}_b$, $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{OR}_c$,
 $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{R}_c$, $\text{NR}_a\text{P}(\text{O})\text{OR}_b\text{OR}_c$, SR_a , $\text{S}(\text{O})\text{R}_a$, $\text{S}(\text{O})_2\text{R}_a$, $\text{S}(\text{O})\text{OR}_a$, $\text{S}(\text{O})_2\text{OR}_a$,
 20 $\text{S}(\text{O})\text{NR}_a\text{R}_b$, $\text{S}(\text{O})_2\text{NR}_a\text{R}_b$, $\text{P}(\text{O})\text{OR}_a\text{OR}_b$, $\text{B}(\text{OH})_2$, halogen, aryl, heteroaryl, biaryl, and
 a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched, cyclic, or unbranched alkyl group; and

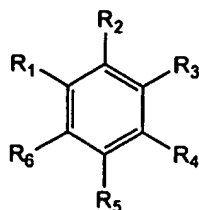
- 25 wherein any of R_1 through R_8 and R_a through R_c may be substituted or unsubstituted.

178. The method according to claim 124, wherein the compound has the following formula:

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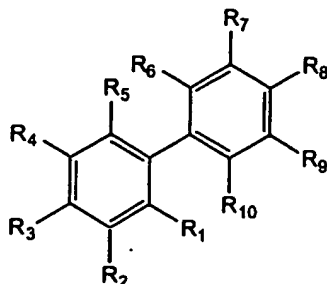
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wherein R_1 through R_6 may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
 10 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
 15 cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_6 and R_a through R_c may be substituted or unsubstituted.

179. The method according to claim 124, wherein the compound has the
 20 following formula:



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wherein R_1 through R_{10} may be the same or different and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$,
5 $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, and a branched, cyclic, or unbranched alkyl group,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, a branched,
10 cyclic, or unbranched alkyl group; and

wherein any of R_1 through R_{10} and R_a through R_c may be substituted or unsubstituted.

180. A method for protecting against or treating hearing loss in a subject
15 comprising administering an effective amount of a protein tyrosine kinase inhibitor to the subject to protect against or to treat hearing loss.

181. The method according to claim 180, wherein the protein tyrosine
20 kinase inhibitor is a non-peptide protein tyrosine kinase inhibitor.

182. The method according to claim 181, wherein the non-peptide protein
tyrosine kinase inhibitor comprises at least one first module having one or more
functional groups each capable of covalently or non-covalently binding to catalytic
residues of the protein kinase and a second module which provides a non-peptide
25 scaffold, wherein the combination of the at least one first module and second module
inhibits protein kinase activity.

183. The method according to claim 182, wherein the at least one first
module comprises two or more functional groups.

30

184. The method according to claim 182, wherein the at least one first
module comprises a functional group selected from the group consisting of a halogen,

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a boronic acid, a hydroxyl group, phosphonic acid, sulfamic acid, a guanidino group, carboxylic acid, an aldehyde, an amide, and hydroxymethylphosphonic acid.

185. The method according to claim 184, wherein the at least one first
5 module comprises a halogen.

186. The method according to claim 184, wherein the at least one first module comprises a boronic acid group.

10 187. The method according to claim 184, wherein the at least one first module comprises a hydroxyl group.

188. The method according to claim 184, wherein the at least one first module comprises an amide group.

15 189. The method according to claim 188, wherein the amide group is a vicinal tricarbonyl amide.

20 190. The method according to claim 182, wherein the second module comprises a group selected from the group consisting of indole, naphthalene, biphenyl, isoquinoline, benzofuran, and benzothiophene.

25 191. The method according to claim 190, wherein the second module comprises an indole.

192. The method according to claim 190, wherein the second module comprises naphthalene.

30 193. The method according to claim 182, wherein the at least one first module further comprises a linear chain comprising between one and three carbon atoms which links the at least one first module to the second module.

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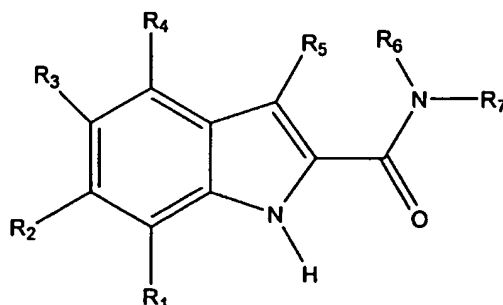
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194. The method according to claim 193, wherein one of the carbon atoms in the linear chain is substituted with a nitrogen, oxygen, or sulfur atom.

195. The method according to claim 182, wherein the non-peptide protein kinase inhibitor comprises one or more specificity side chain elements attached to the combination of the at least one first module and second module.

196. The method according to claim 182, wherein the non-peptide protein tyrosine kinase inhibitor has the formula:



wherein R_1 through R_7 may be the same or different, and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and branched, cyclic, or unbranched alkyl,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; or

R_5 and R_6 together form a heterocyclic compound; and

wherein any of R_1 through R_7 and R_a through R_c is substituted or unsubstituted.

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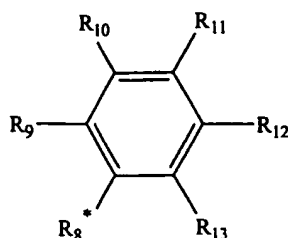
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197. The method according to claim 196, wherein R_3 is a halogen.

198. The method according to claim 197, wherein R_3 is fluorine.

5 199. The method according to claim 196, wherein at least one of R_6 or R_7 is



wherein R_8^* is the point of attachment and is $(CH_2)_x$, wherein x is from 0 to 10, CH_2CHOH , $CH(CH_3)R$, or $CH(CH_3)S$, and each of R_9 through R_{13} may be the same or different, and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$, $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and branched, cyclic, or unbranched alkyl,

wherein R_a , R_b , and R_c may be the same or different and are selected from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl; and

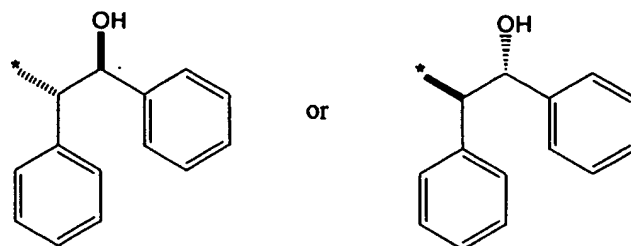
20 wherein any of R_9 through R_{13} and R_a through R_c is substituted or unsubstituted.

200. The method according to claim 196, wherein at least one of R_6 or R_7 is

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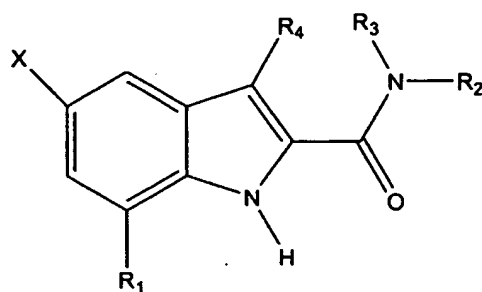
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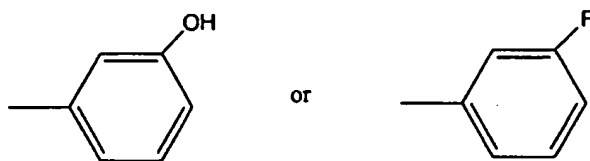


wherein the asterisk indicates the point of attachment to the nitrogen.

201. The method according to claim 182, wherein the non-peptide tyrosine
5 kinase inhibitor has the formula:



wherein X is a halogen, R₁ is H, R₂ is



R₃ is H, and R₄ is H.

10

202. The method according to claim 201, wherein X is fluorine.

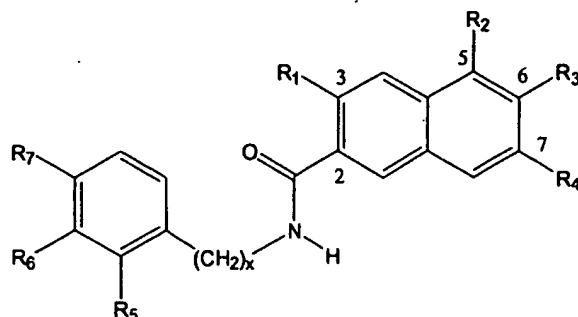
203. The method according to claim 182, wherein the non-peptide tyrosine
kinase inhibitor has the formula

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wherein R_1 through R_7 may be the same or different, and are selected from the group consisting of H, $C(O)R_a$, $C(O)NR_aR_b$, $C(O)OR_a$, $C(O)SR_a$, OH, OR_a , $OC(O)R_a$, $OC(O)OR_a$, NH_2 , NR_aR_b , $NR_aC(O)R_b$, $NR_aC(O)NR_bR_c$, $NR_aC(O)OR_b$, $NR_aC(O)SR_b$,
 5 $NR_aS(O)R_b$, $NR_aS(O)_2R_b$, $NR_aS(O)OR_b$, $NR_aS(O)_2OR_b$, $NR_aP(O)OR_bOR_c$, $NR_aP(O)OR_bR_c$, $NR_aP(O)OR_bOR_c$, SR_a , $S(O)R_a$, $S(O)_2R_a$, $S(O)OR_a$, $S(O)_2OR_a$, $S(O)NR_aR_b$, $S(O)_2NR_aR_b$, $P(O)OR_aOR_b$, $B(OH)_2$, halogen, aryl, heteroaryl, biaryl, heterobiaryl, heterocyclic compound, and branched, cyclic, or unbranched alkyl,

wherein R_a , R_b , and R_c may be the same or different and are selected
 10 from the group consisting of H, aryl, heteroaryl, biaryl, heterobiaryl, and branched, cyclic, or unbranched alkyl;

wherein any of R_1 through R_7 and R_a through R_c is substituted or unsubstituted; and

wherein X is 0 or 1.

15

204. The method according to claim 180, wherein the protein tyrosine kinase inhibitor is a peptide protein tyrosine kinase inhibitor.

205. The method according to claim 180, wherein the protein tyrosine
 20 kinase inhibitor inhibits protein tyrosine kinase activity but does not inhibit ATP binding to the protein tyrosine kinase.

206. The method according to claim 205, wherein the protein tyrosine kinase inhibitor is a peptide substrate directed inhibitor.

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207. The method according to claim 180, wherein the protein tyrosine kinase inhibitor is a SH2 inhibitor.

208. The method according to claim 180, wherein the protein tyrosine
5 kinase inhibitor is a SH3 inhibitor.

209. The method according to claim 180, wherein the protein tyrosine kinase inhibitor is an allosteric inhibitor.

10 210. The method according to claim 180, wherein the protein tyrosine kinase inhibitor inhibits ATP binding to the protein tyrosine kinase.

211. The method according to claim 180, wherein the protein tyrosine kinase is a Src family protein tyrosine kinase.
15

212. The method according to claim 211, wherein the Src family protein tyrosine kinase is pp60^{c-src} tyrosine kinase.

213. The method according to claim 180, wherein the protein tyrosine
20 kinase is focal adhesion kinase.

214. The method according to claim 180, wherein the administering is carried out orally, parenterally, subcutaneously, intravenously, intramuscularly, intraperitoneally, by intranasal instillation, by intracavitary or intravesical instillation,
25 intraauditorily, intraarterially, intralesionally, by metering pump, or by application to mucous membranes.

215. The method according to claim 180, wherein protein tyrosine kinase inhibitor is administered with a pharmaceutically acceptable carrier.
30

216. The method according to claim 180, wherein the protein tyrosine kinase inhibitor is administered before initiation of hearing loss.

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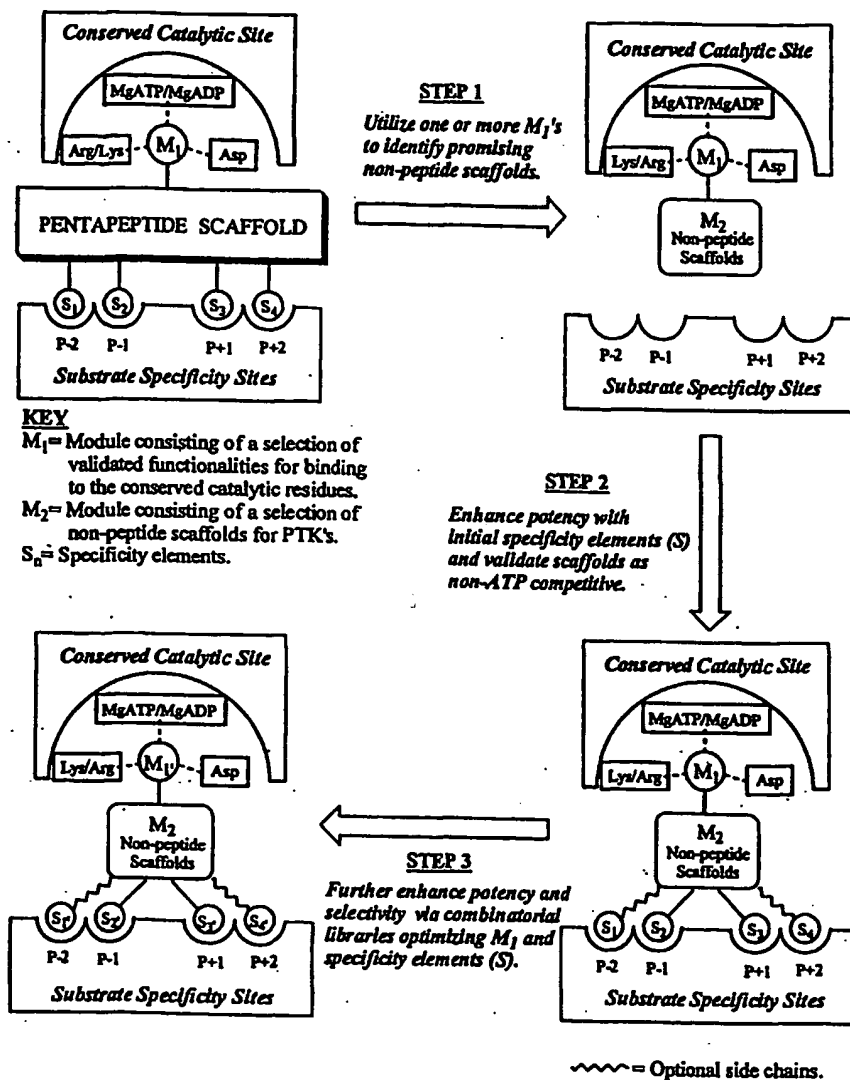
217. The method according to claim 180, wherein the protein tyrosine kinase inhibitor is administered after initiation of hearing loss.

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Figure 1

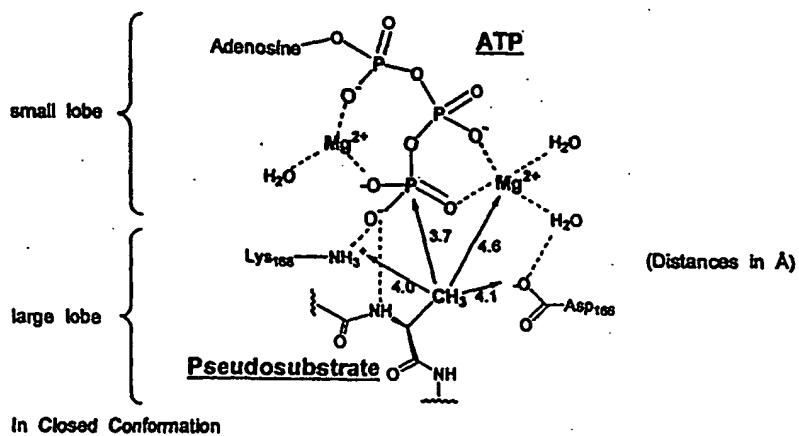
MODULAR STRATEGY FOR DEVELOPING NON-PEPTIDE PROTEIN KINASE INHIBITORS



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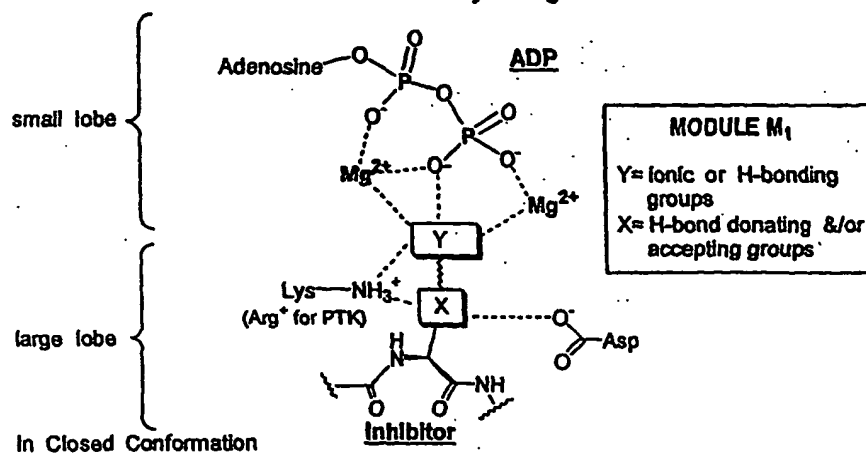
Figure 2
x-ray structure of (PKA):Mg₂ATP:pseudosubstrate inhibitor



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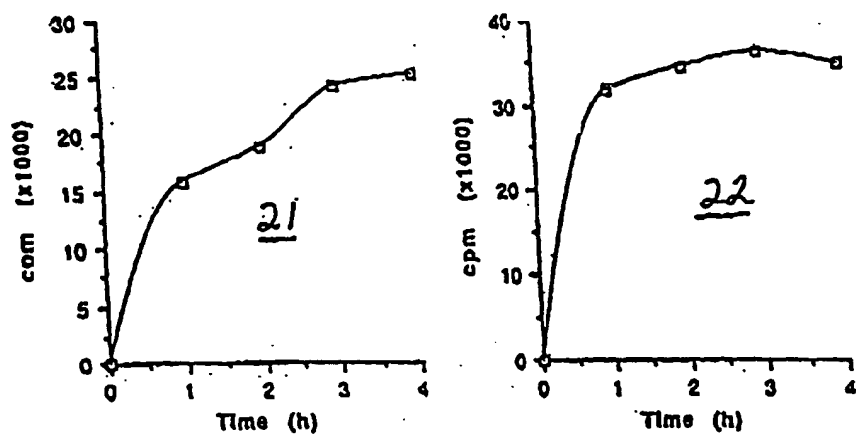
Figure 3

General Module M₁ Design Features For Binding To The Conserved Protein Kinase Catalytic Region

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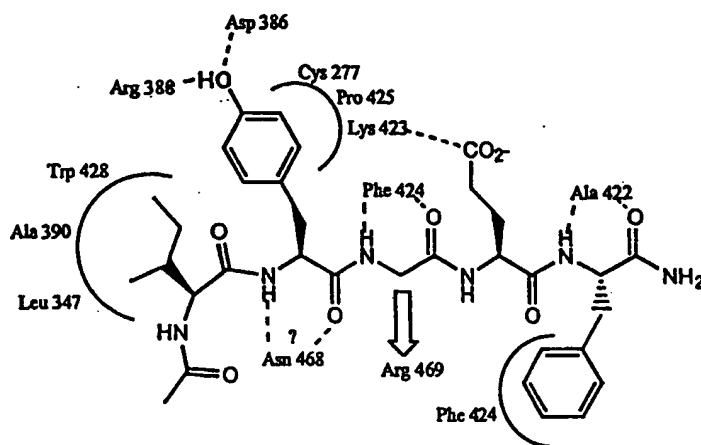
Figure 4
SUBSTRATE BEHAVIOR FOR BORONIC ACID PKA INHIBITORS 21 & 22



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Figure 5
Binding interactions of src substrate
Ac-Ile-Tyr-Gly-Glu-Phe-NH₂ in model src active site.

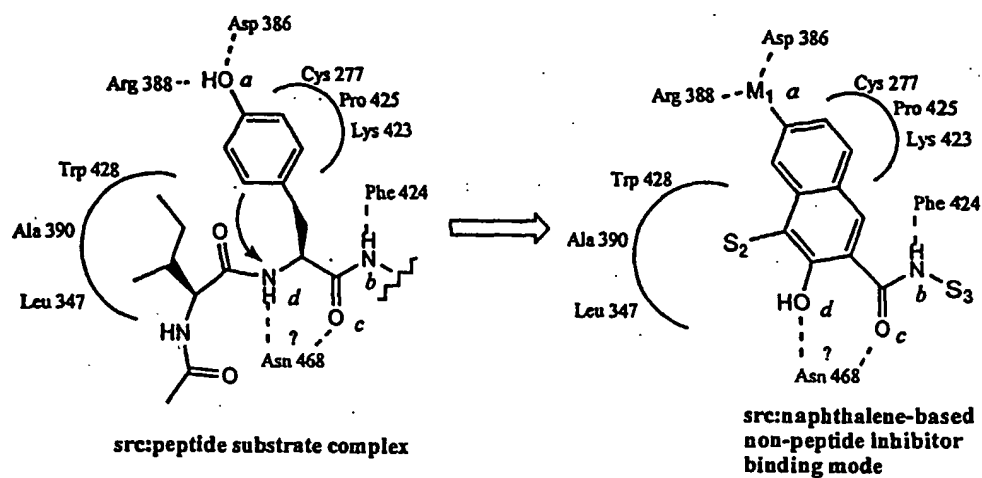


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Figure 6

Design of naphthalene-based src inhibitor scaffold

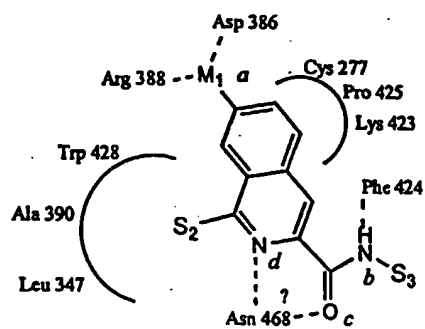


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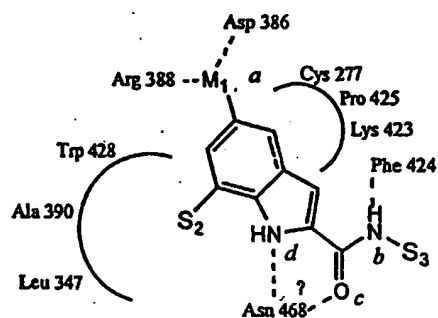
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Figure 7

Design of isoquinoline and indole-based src inhibitor scaffolds



src:isoquinoline-based
non-peptide inhibitor
binding mode

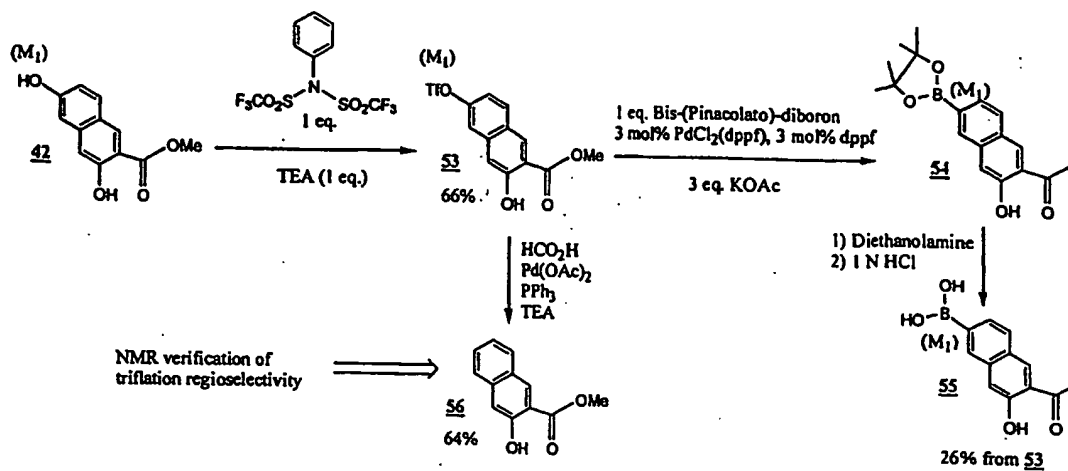


src:indole-based
non-peptide inhibitor
binding mode

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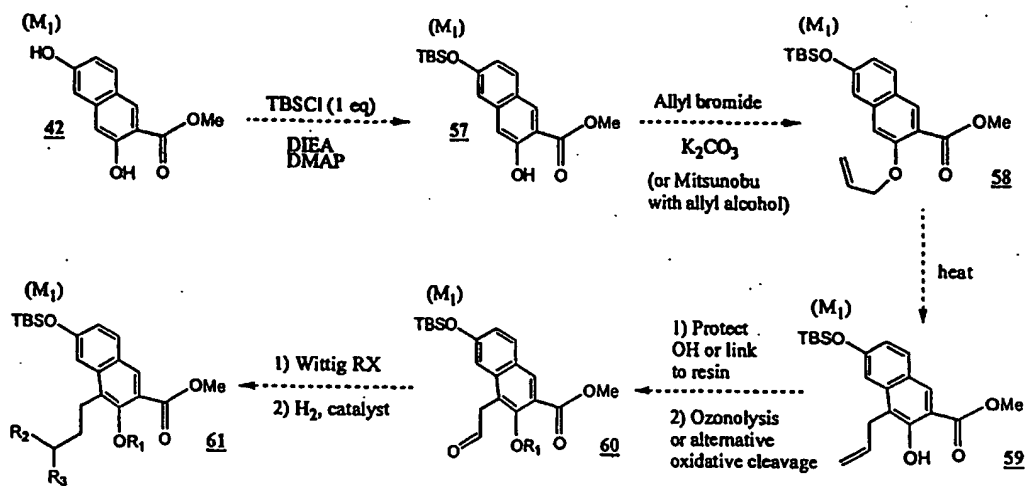
Figure 8



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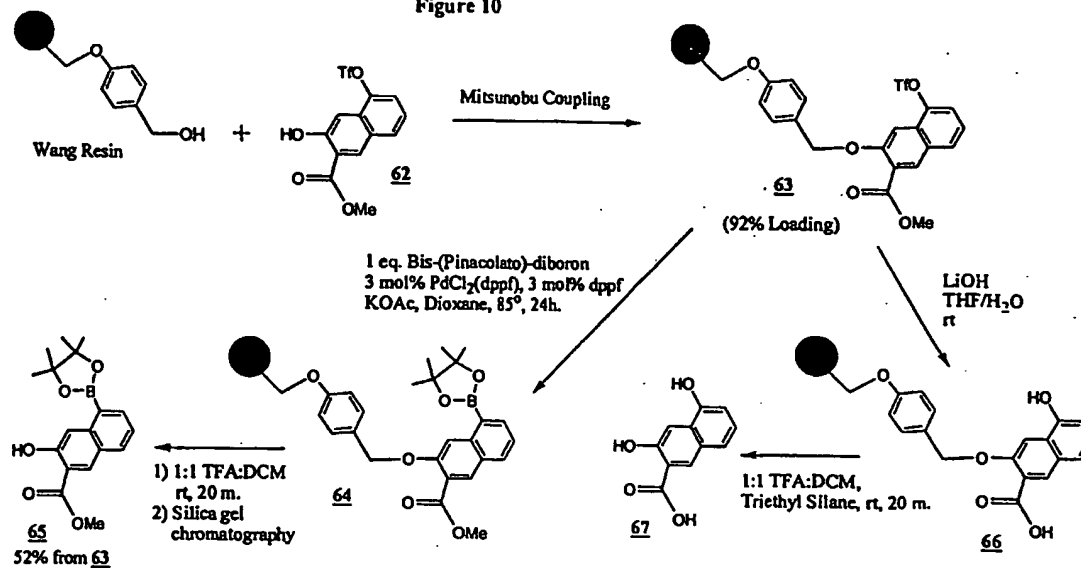
Figure 9



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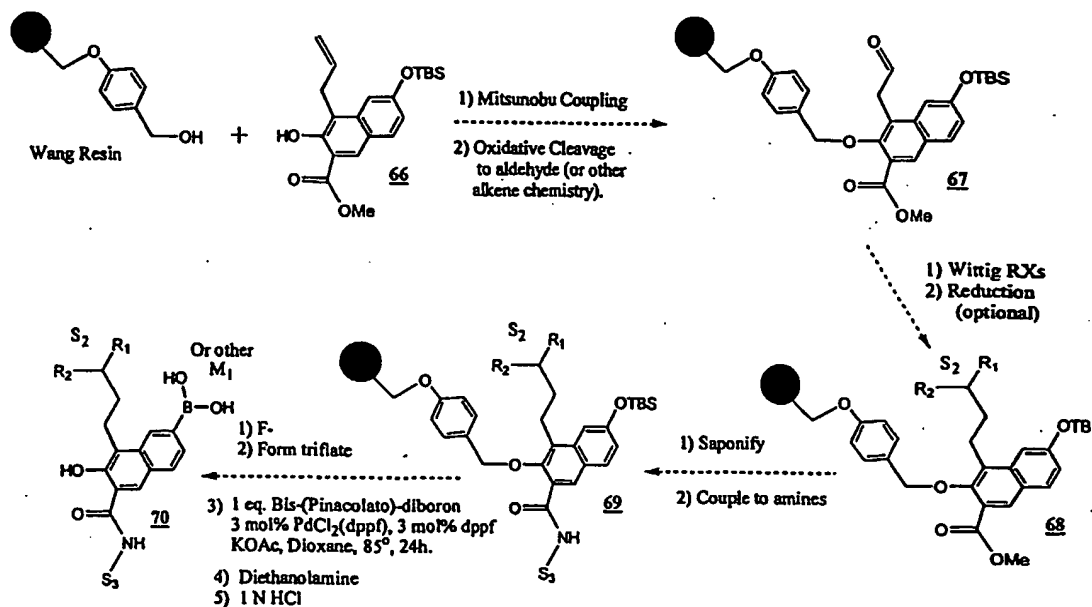
Figure 10



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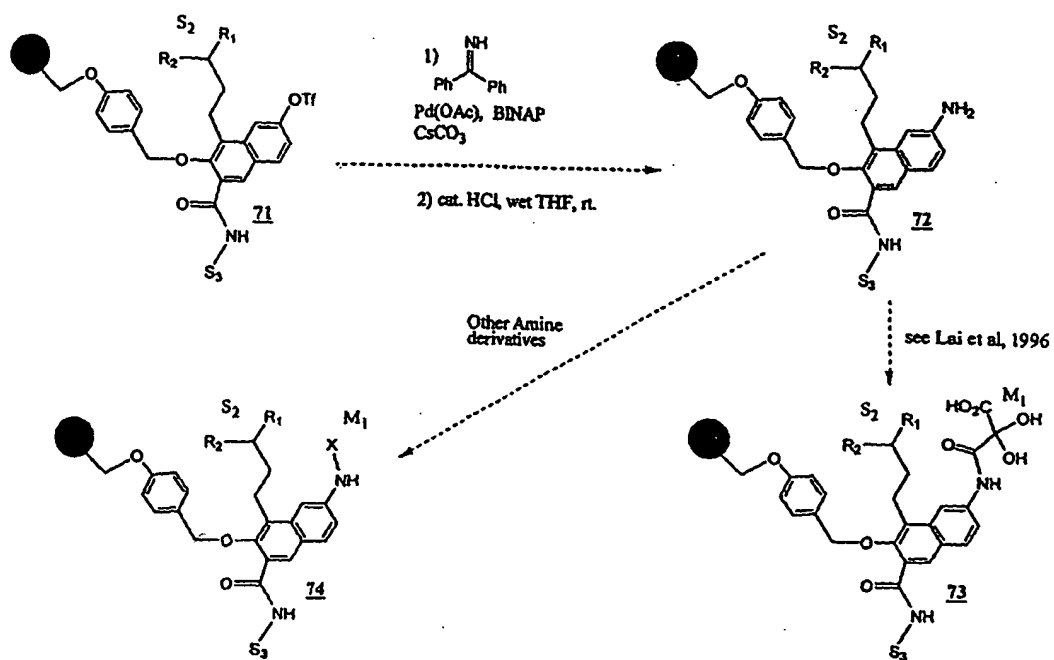
Figure 11



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Figure 12

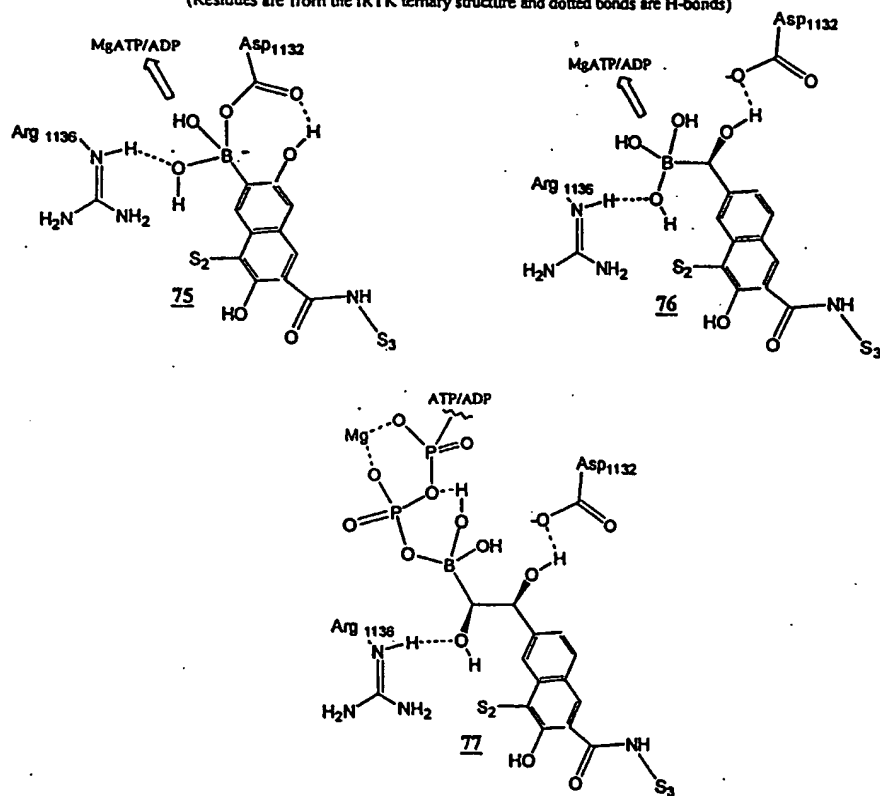


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Figure 13

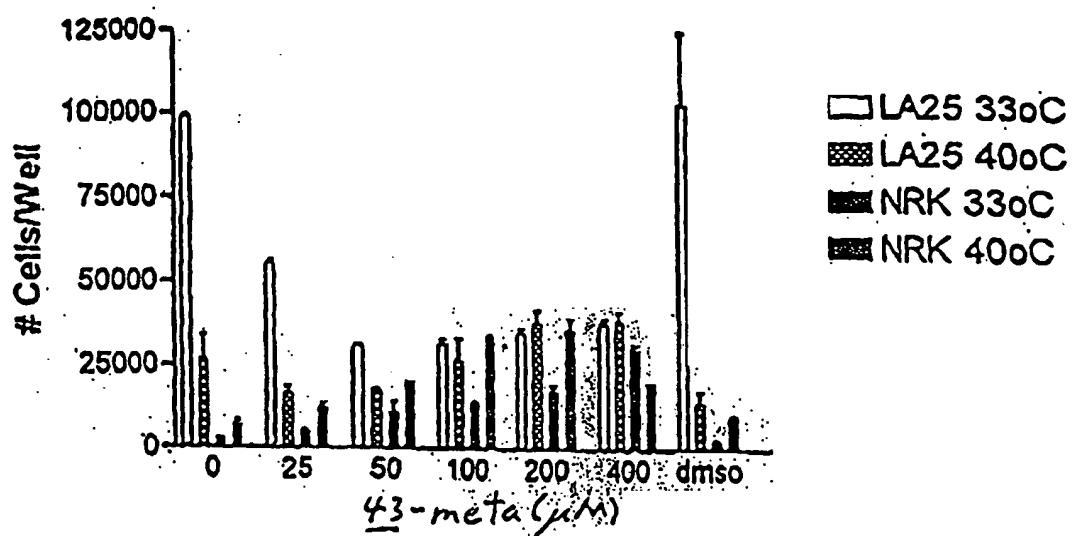
(Residues are from the IR1K ternary structure and dotted bonds are H-bonds)



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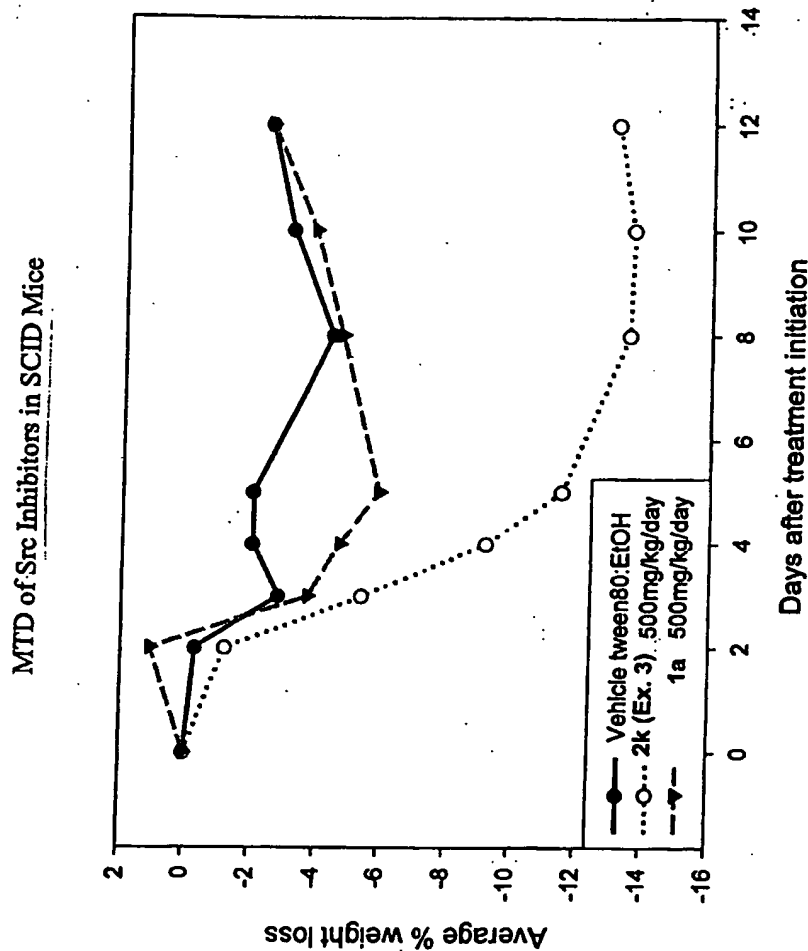
FIGURE 14



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FIGURE 15

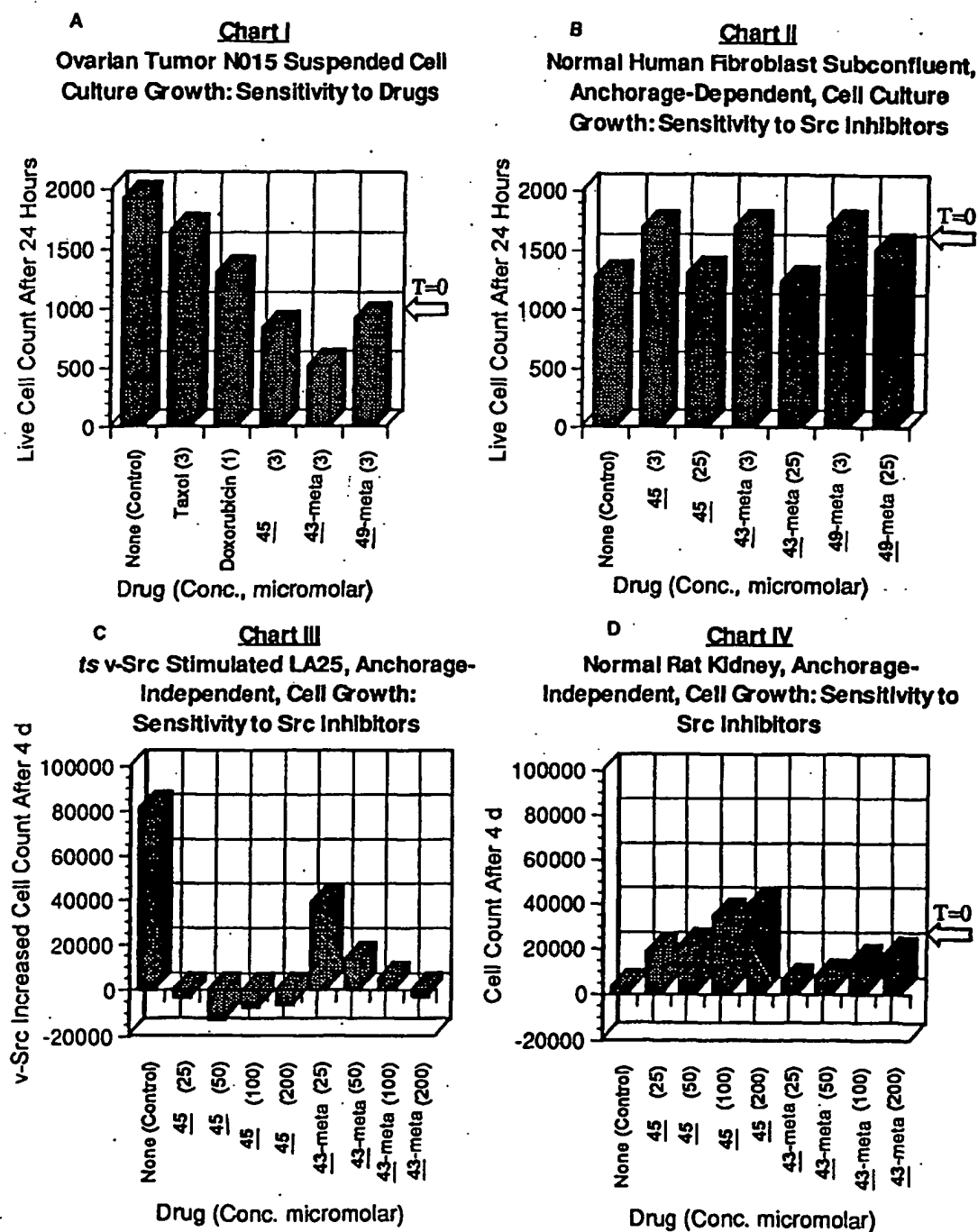


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FIGURE 1a

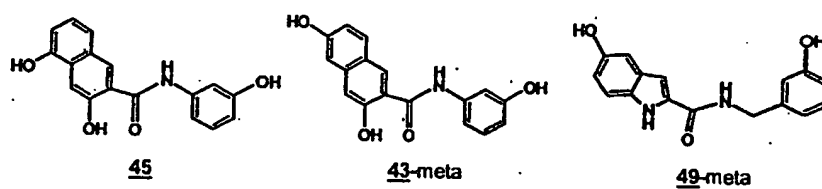
SRC INHIBITOR'S EFFECT ON TRANSFORMED CELL GROWTH AND LACK OF TOXICITY IN NORMAL CELLS



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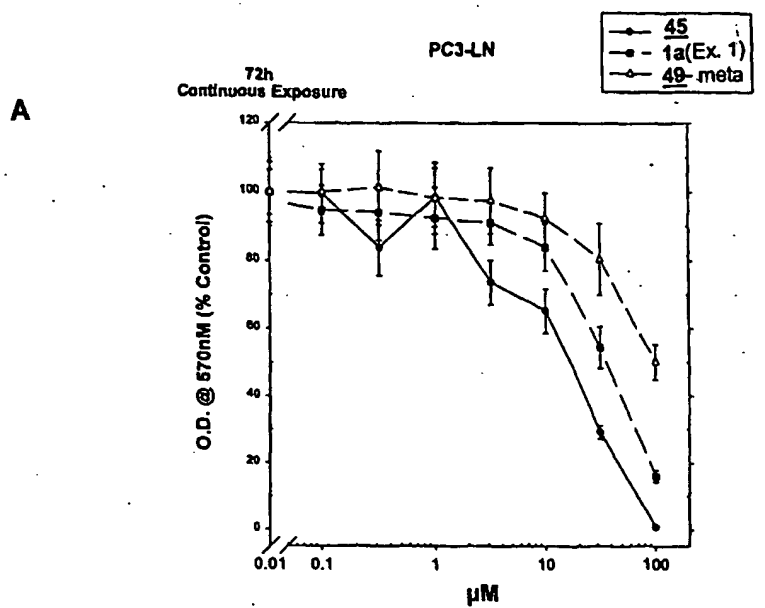
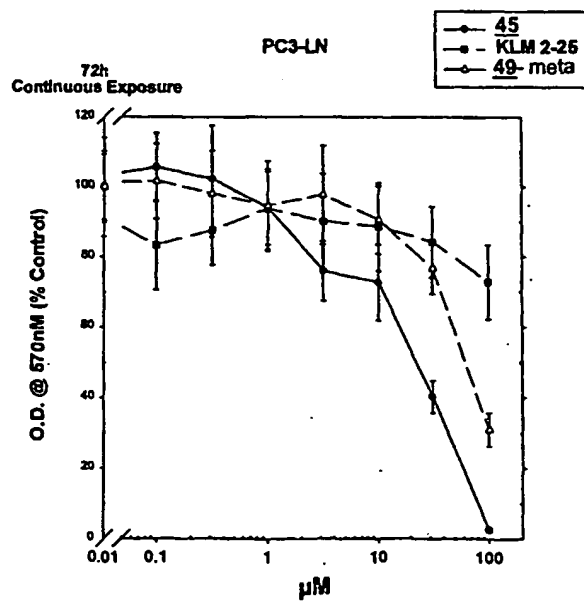
FIGURE 16E



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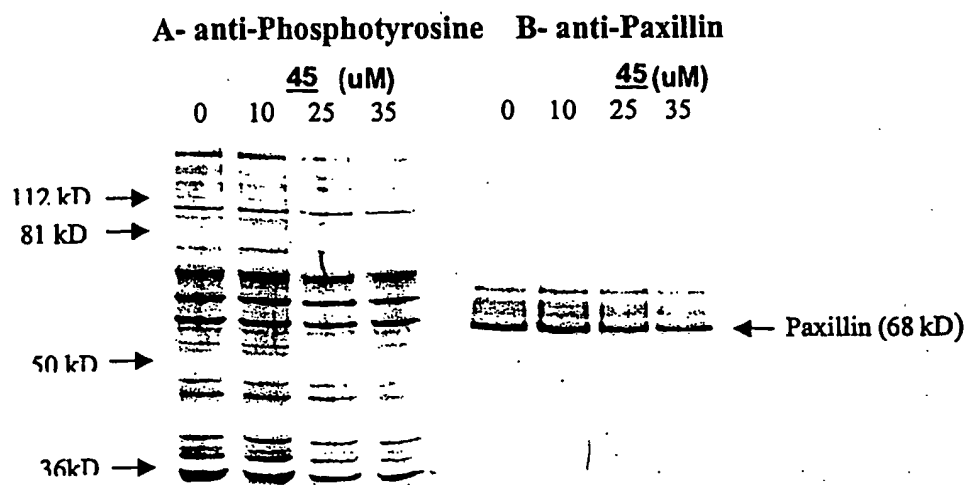
Figure 17

**B**

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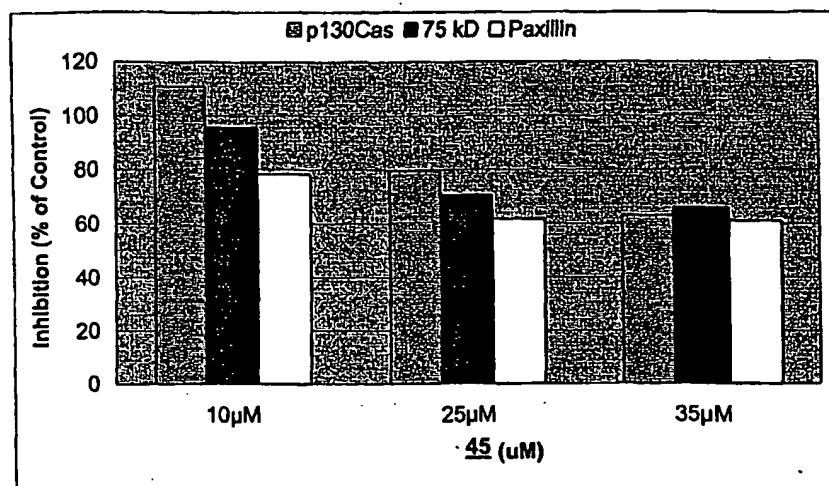
Figure 18



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Figure 19

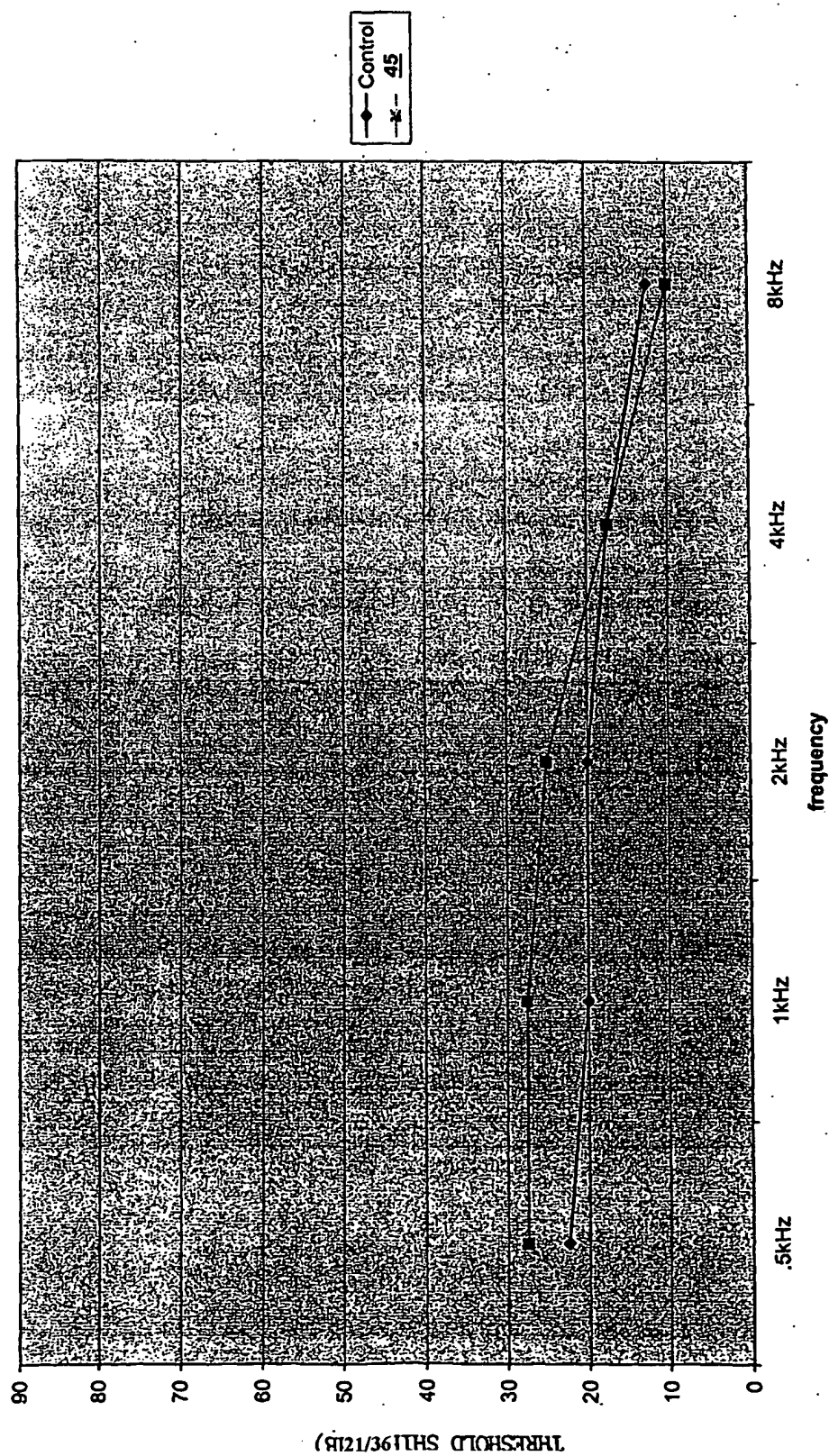


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Figure 20

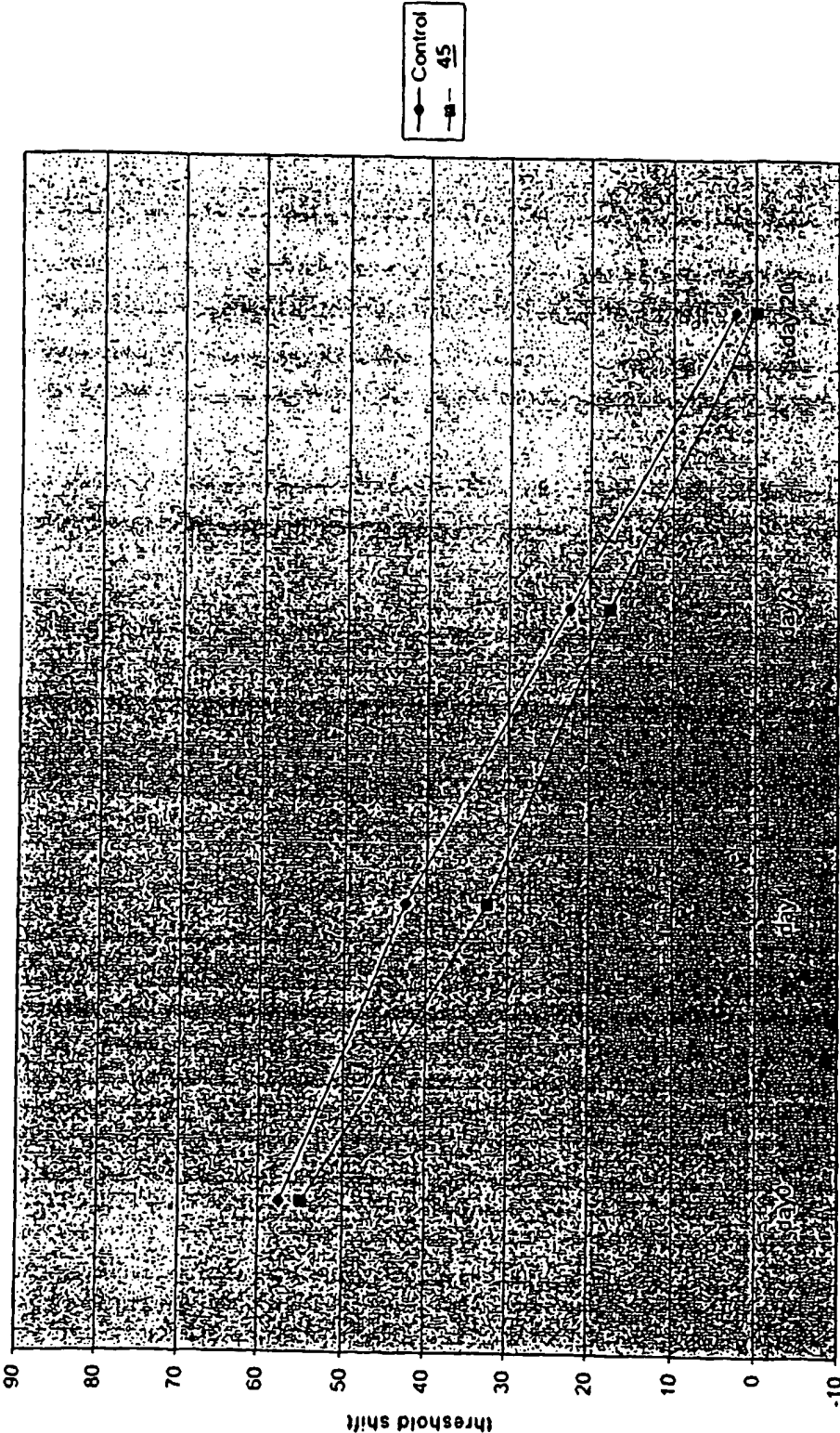
Pretest thresholds



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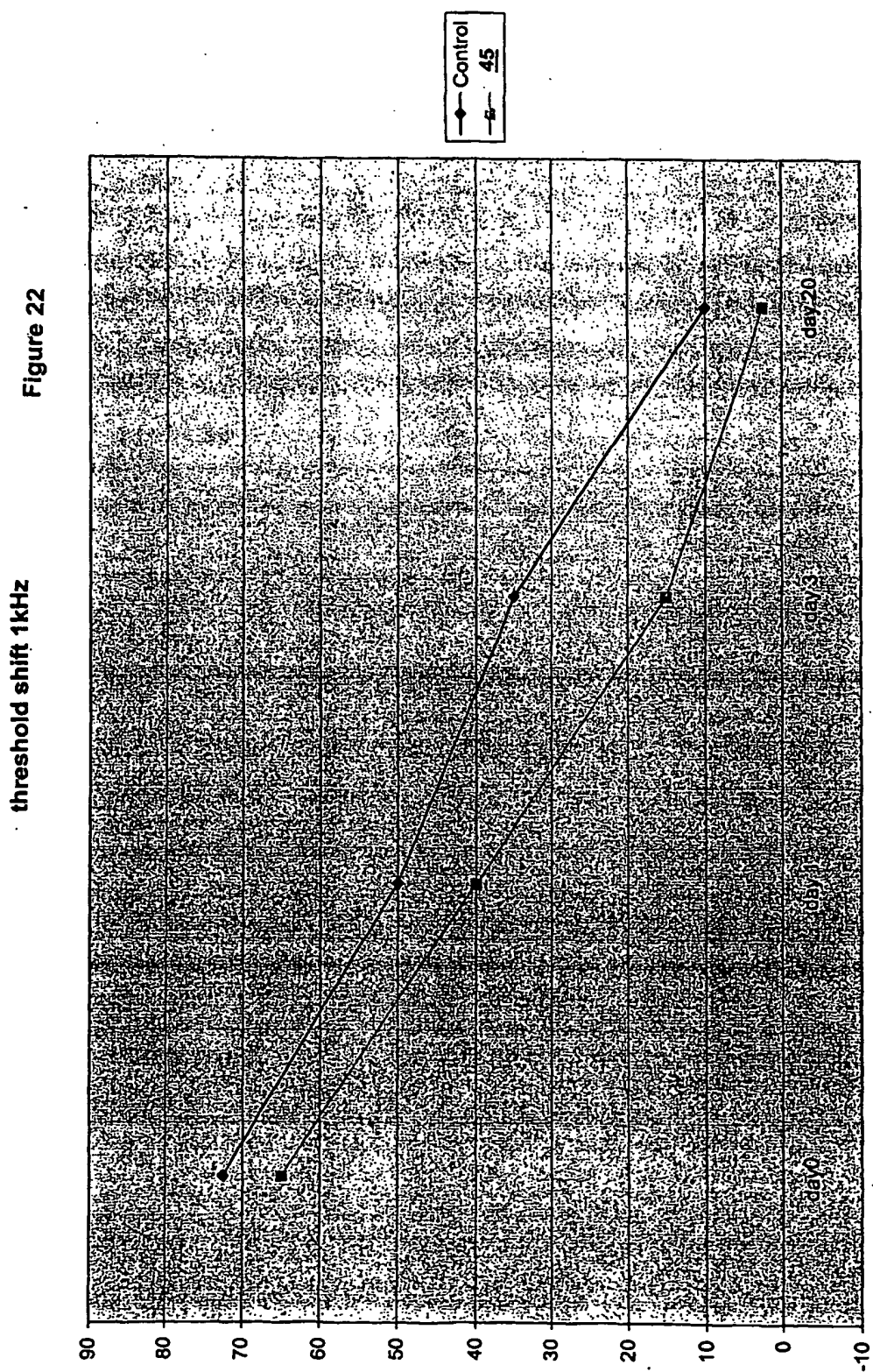
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Figure 21
Threshold shift .5kHz



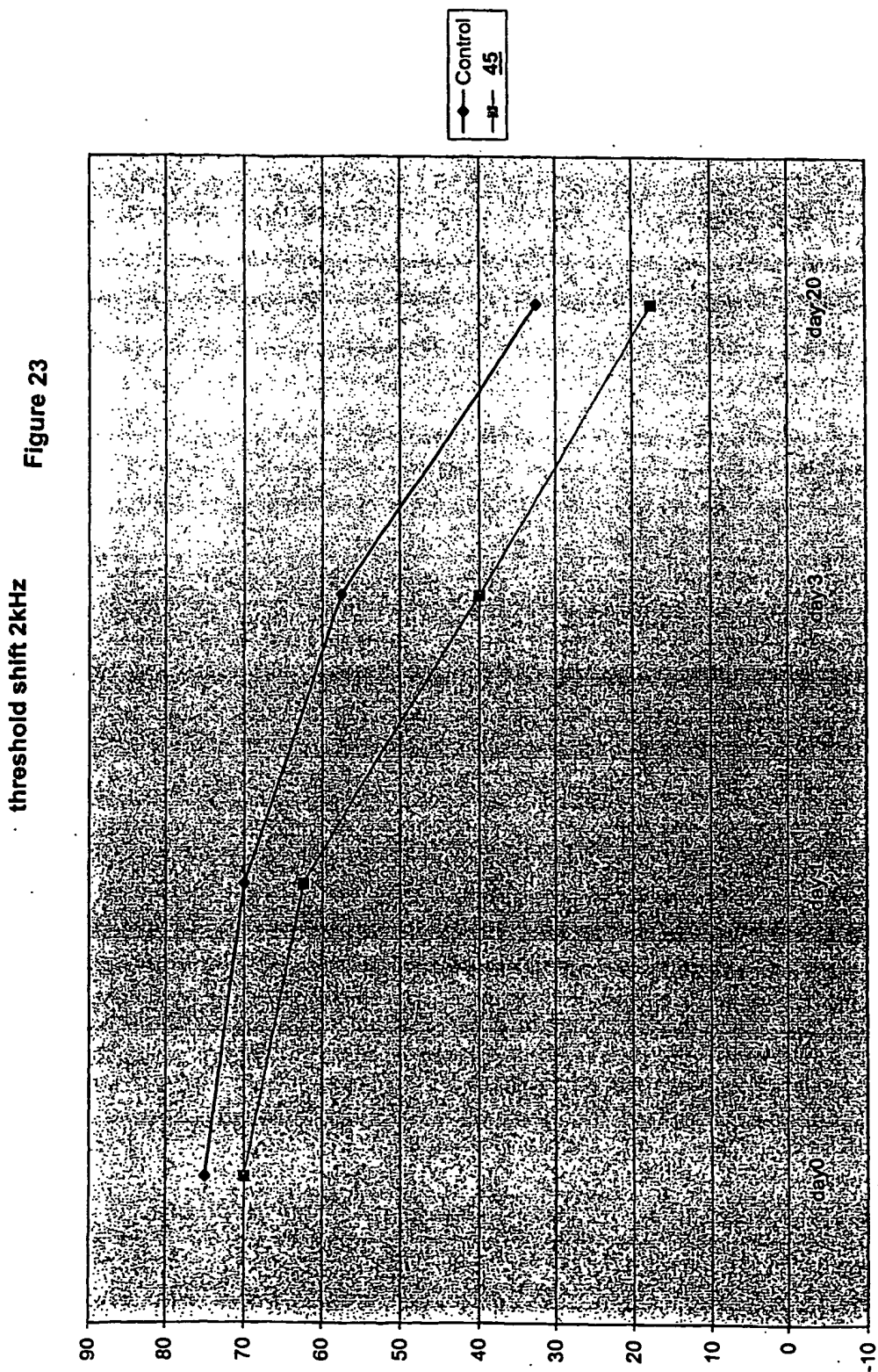
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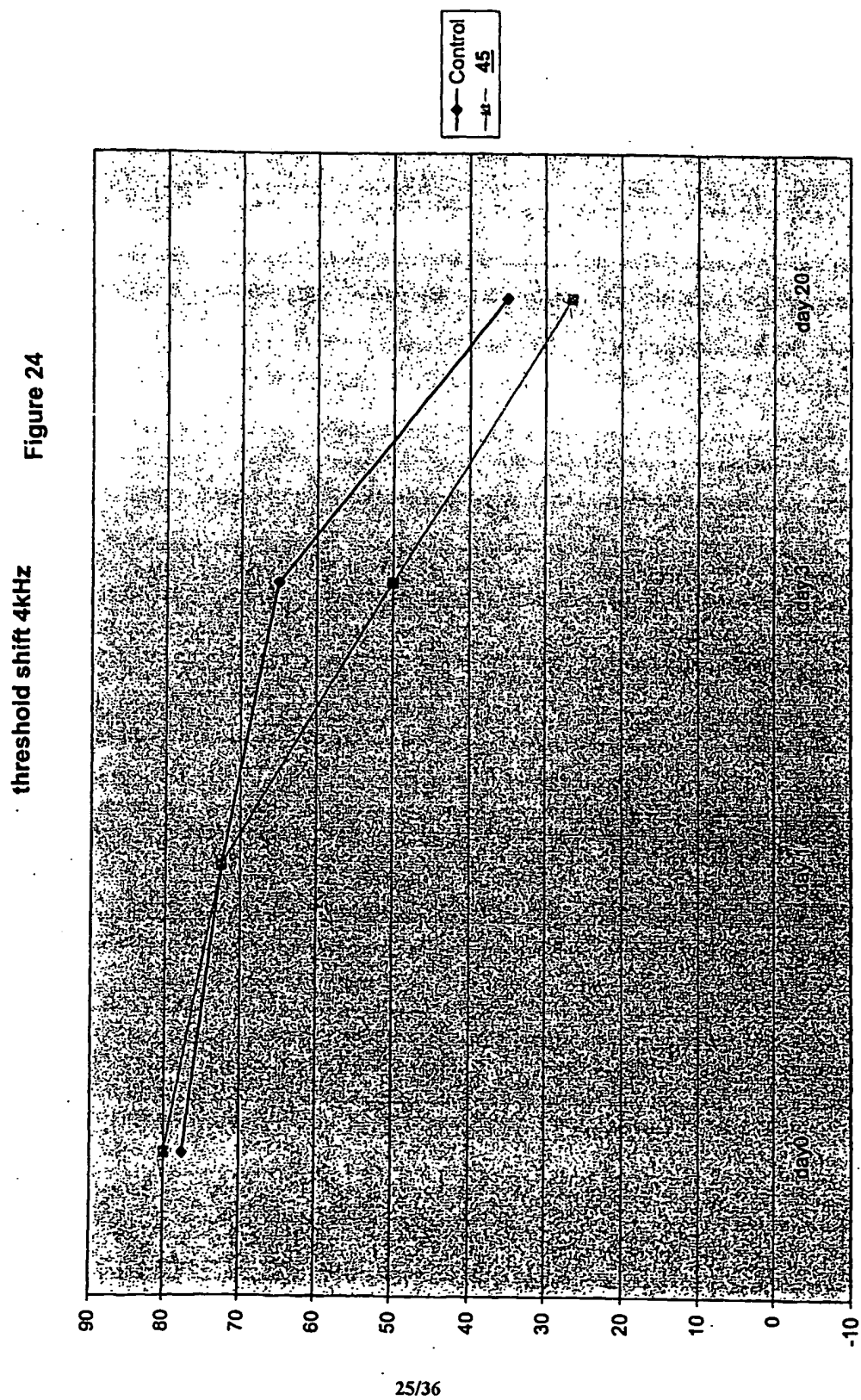
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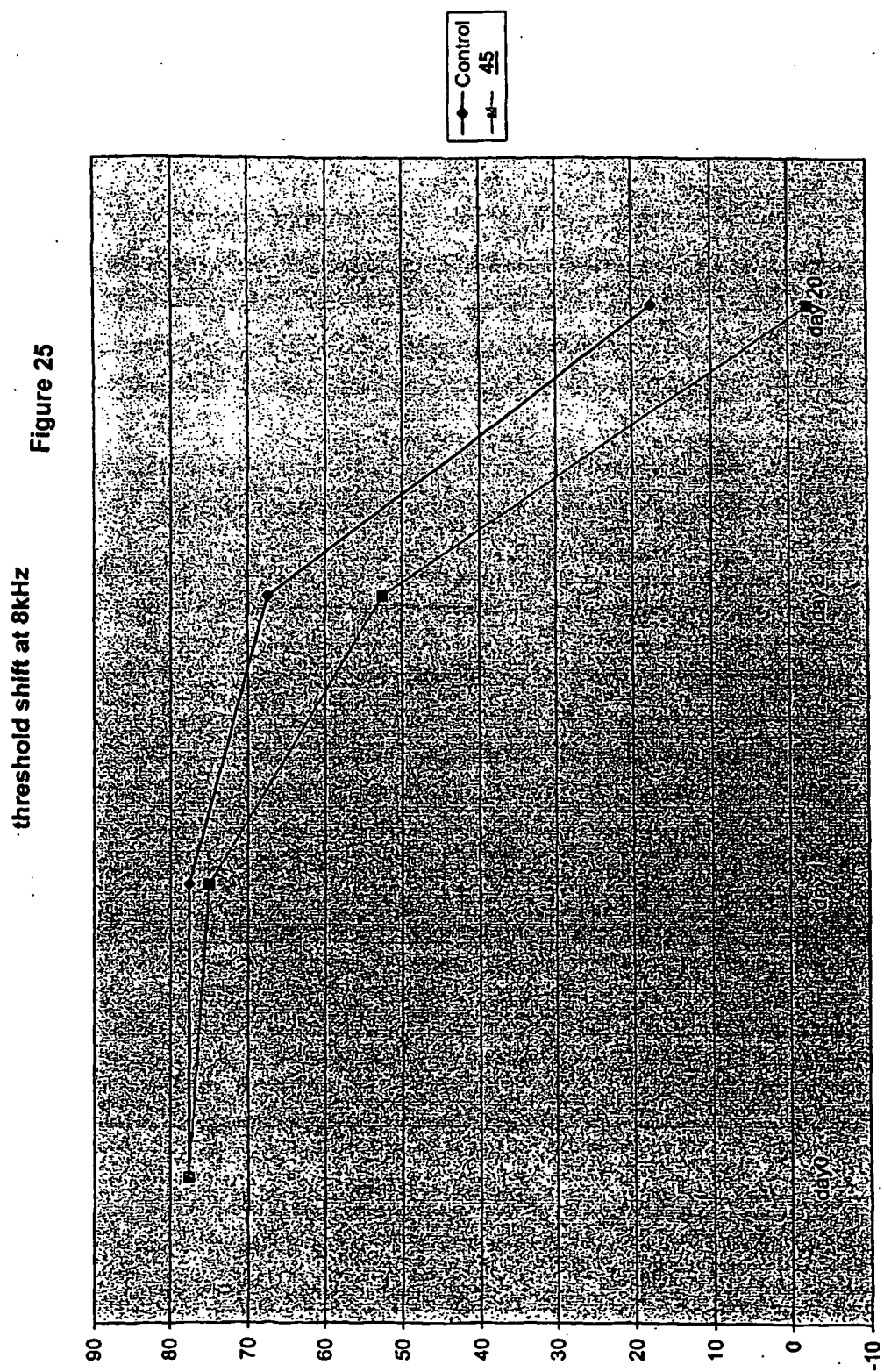
WO 03/035621

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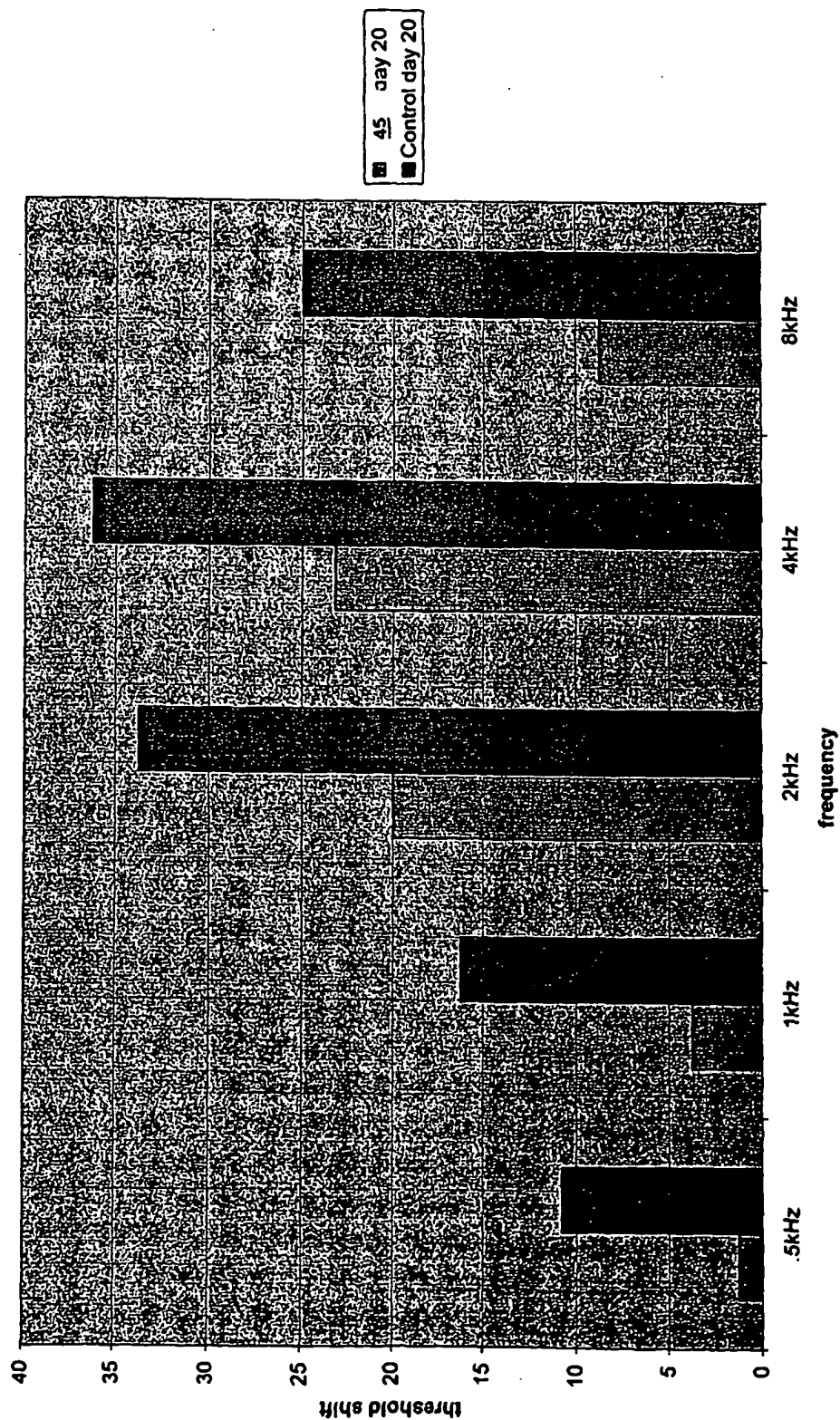


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Figure 26

45 PTS n=4

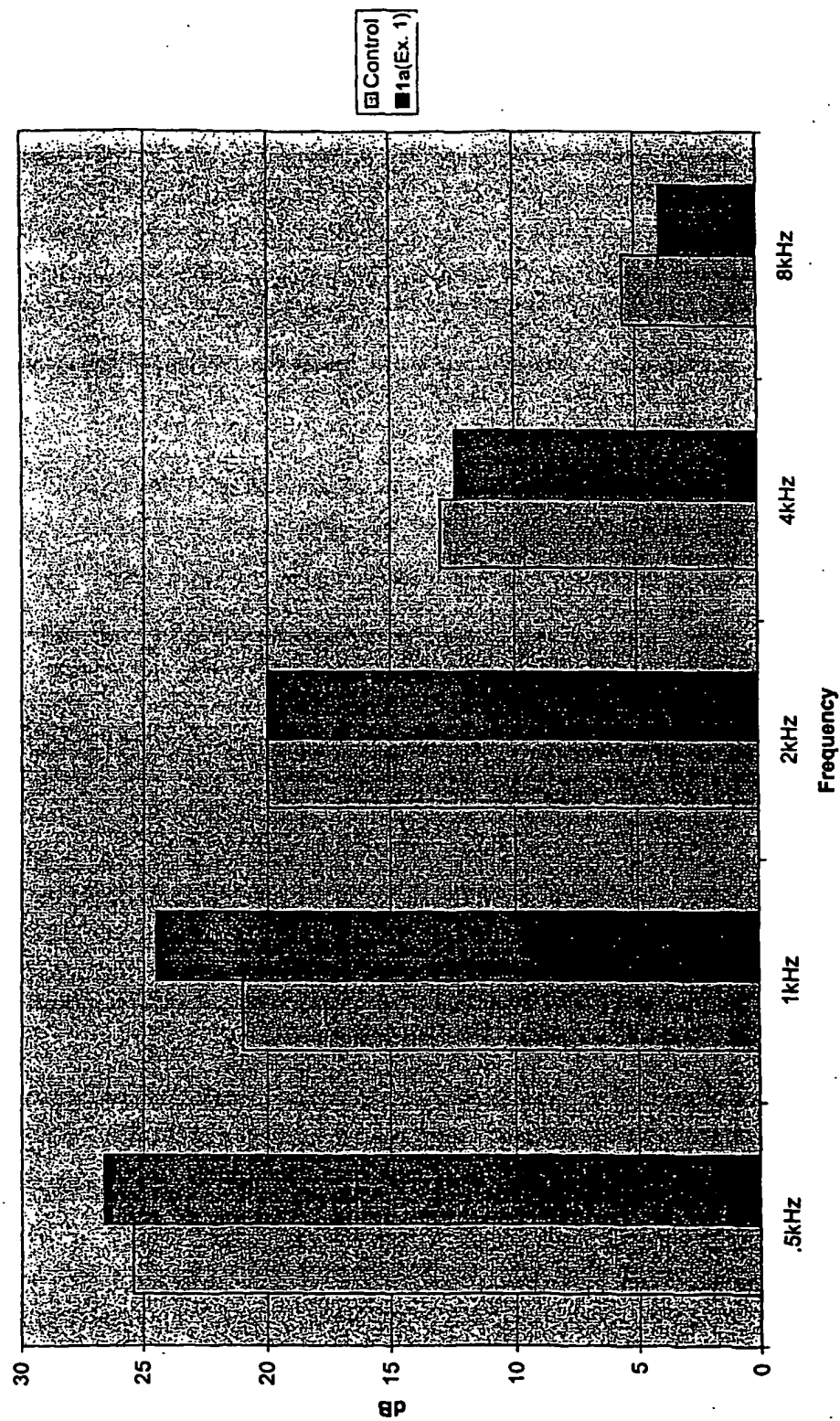


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Figure 27

Pretest n=5

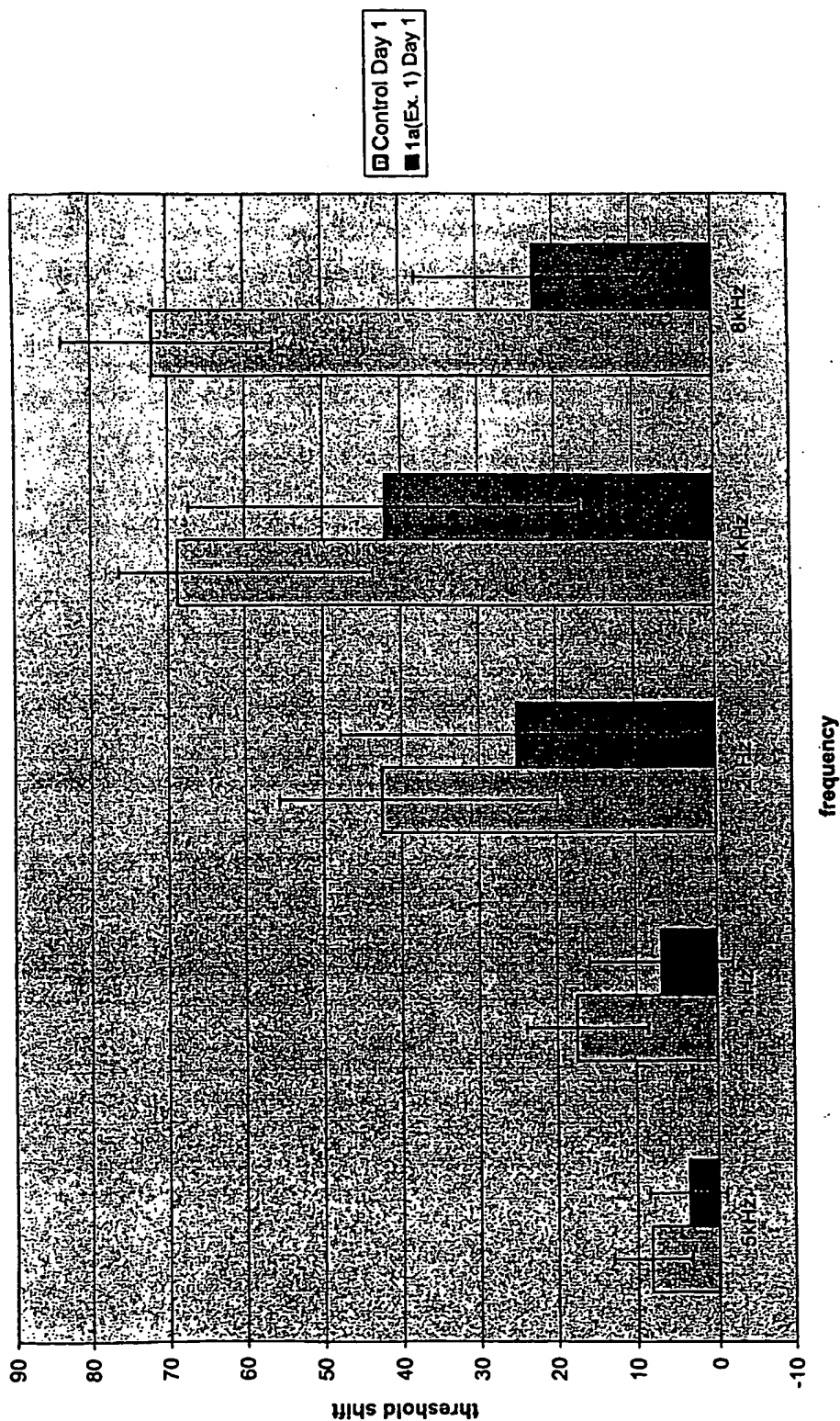


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Figure 28

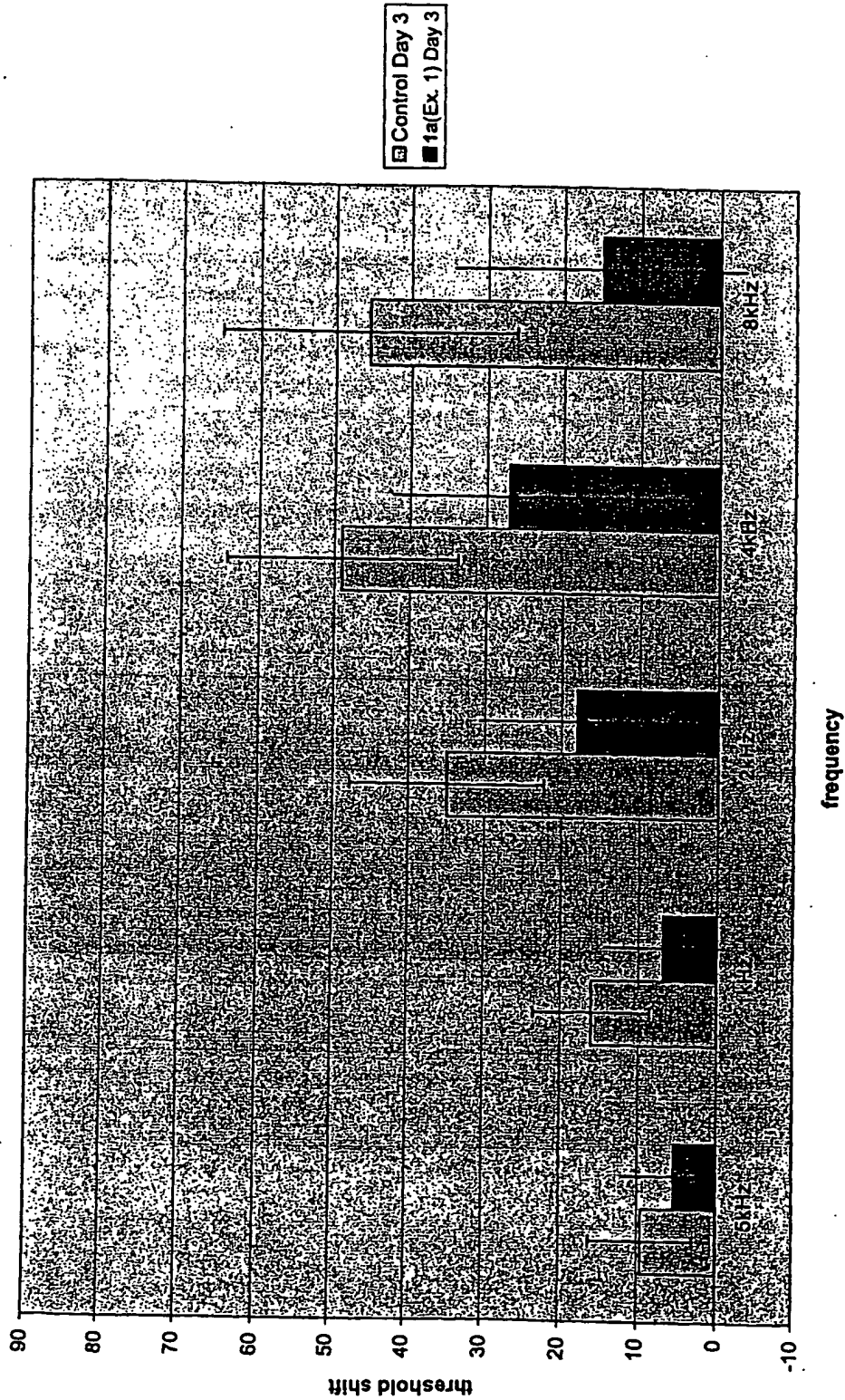
Day1 n=4



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Day 3 n=5
Figure 29

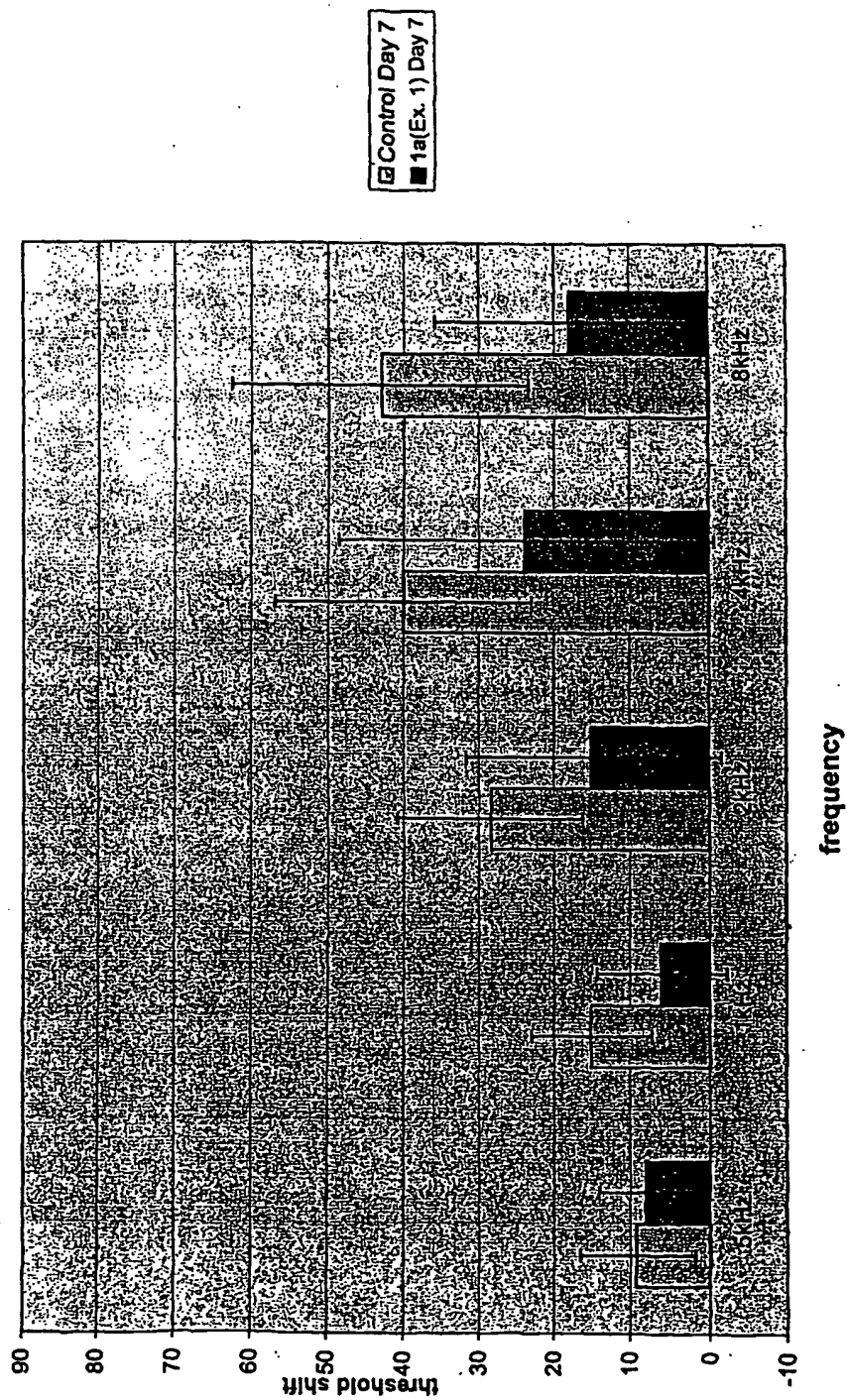


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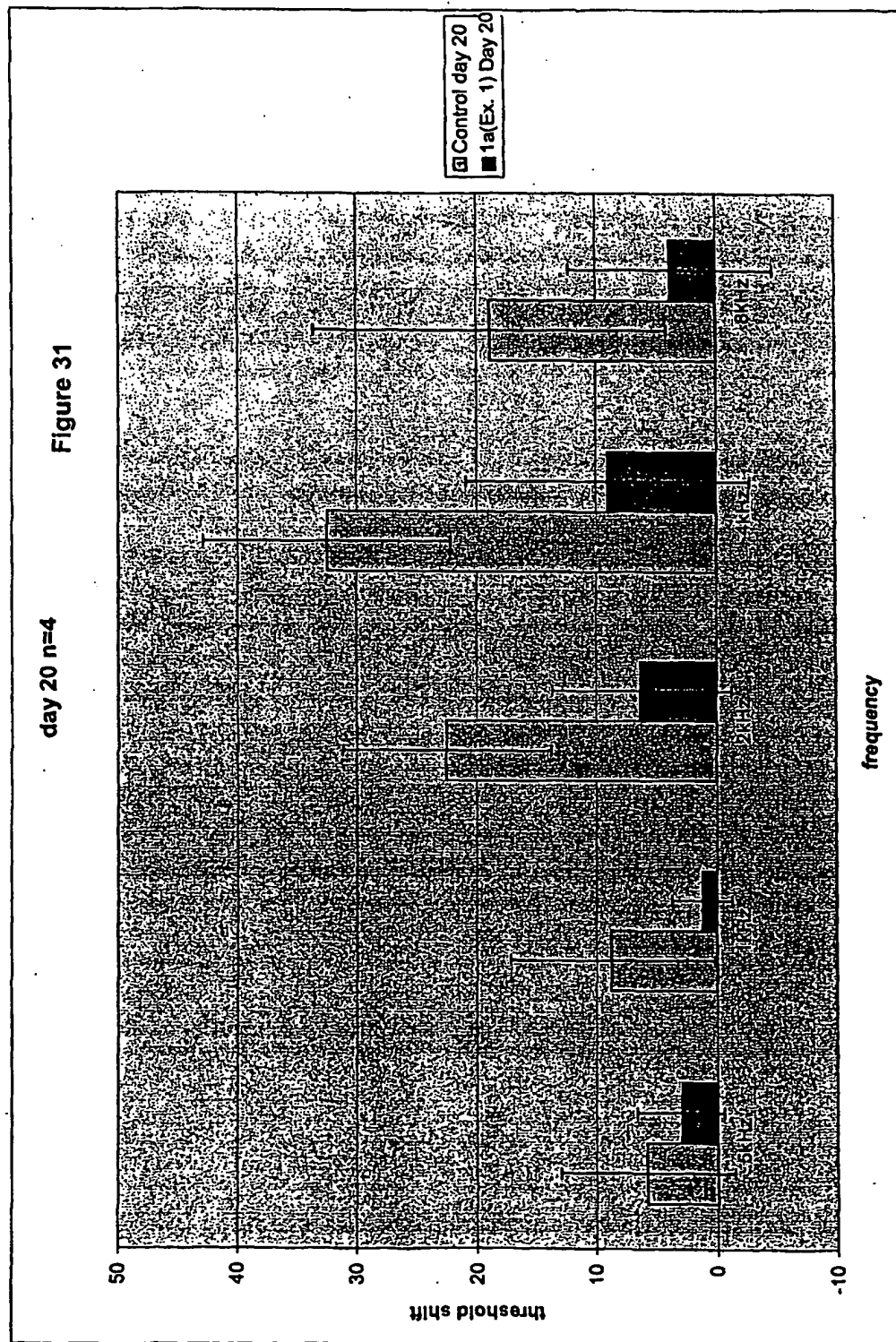
Figure 30

Day 7 n=5



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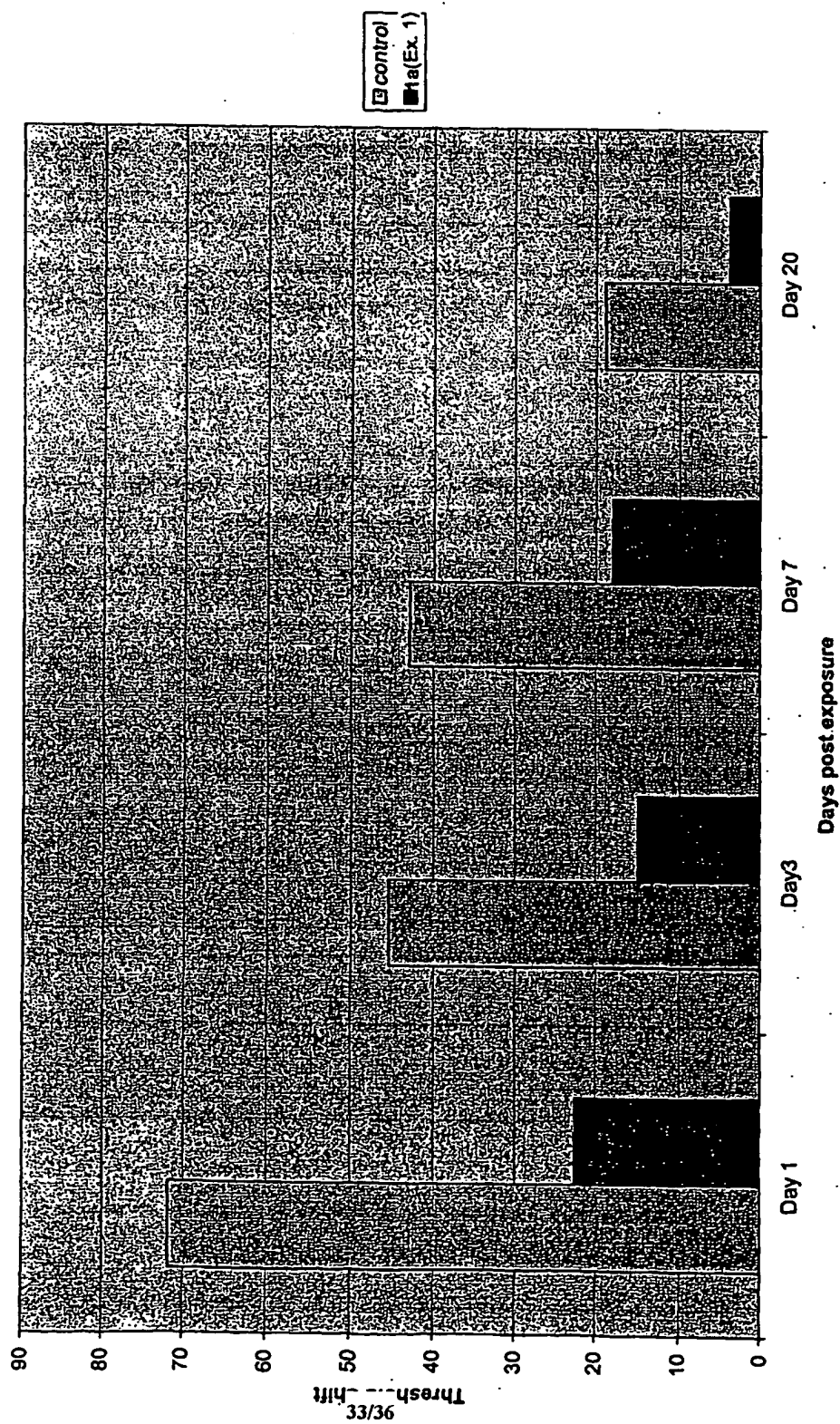


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Figure 32

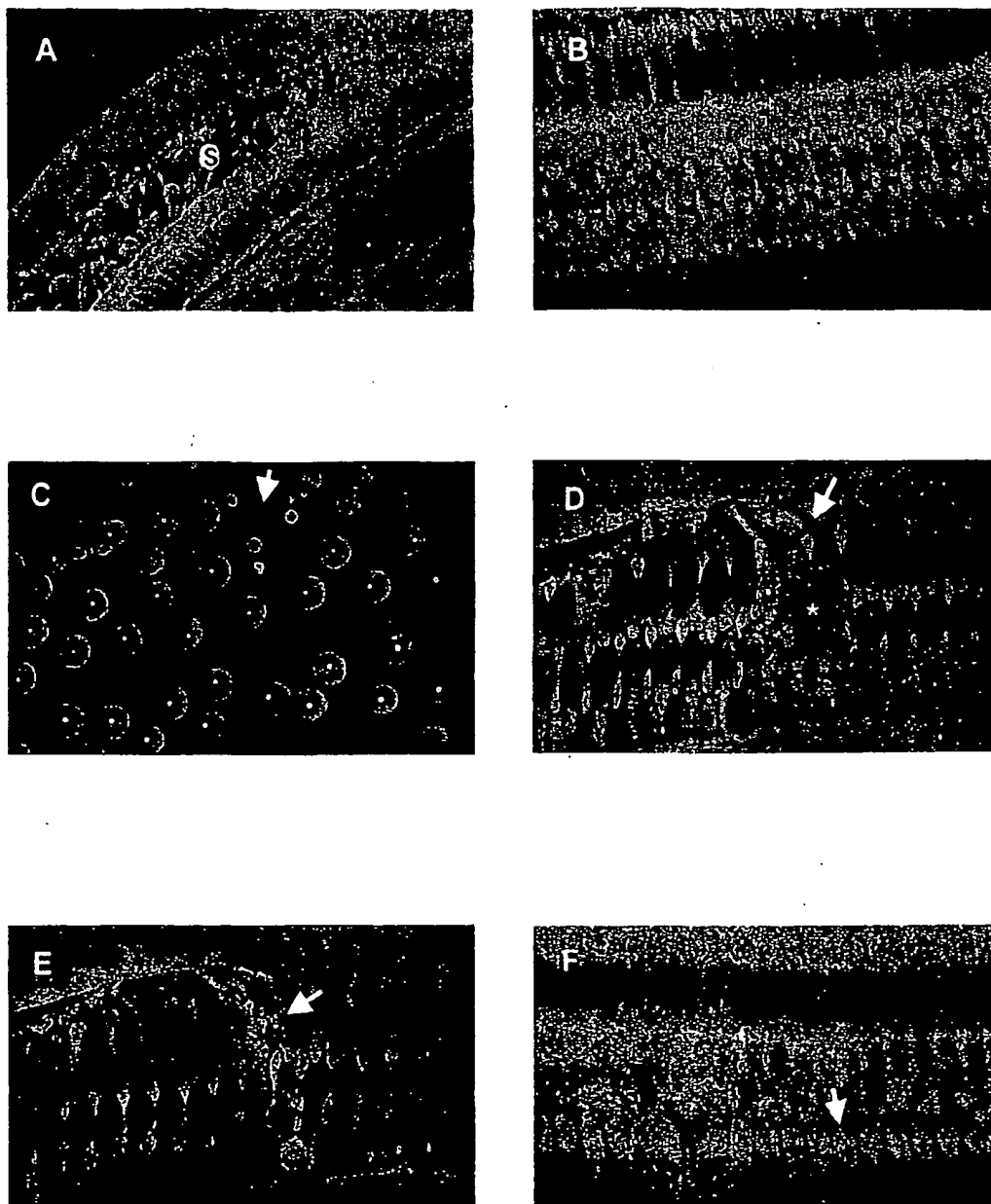
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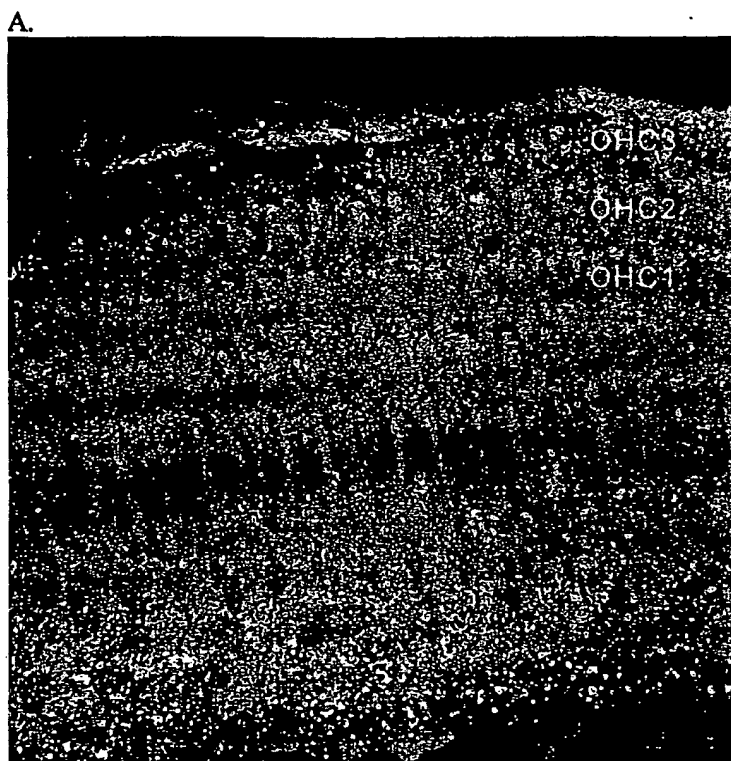
Figure 33



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Figure 34A

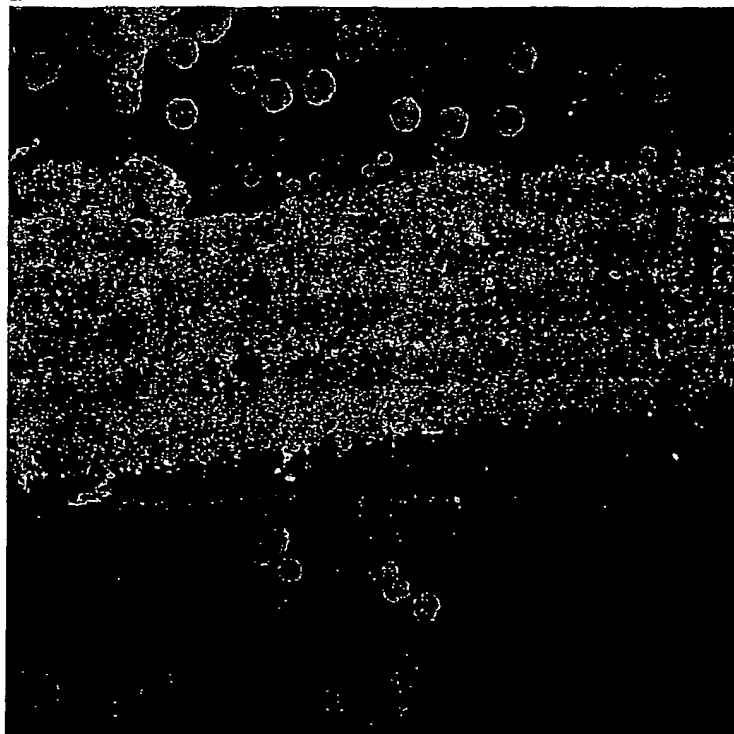


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Figure 34B

B.



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SEQUENCE LISTING

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Roswell Park Cancer Institute

<120> PROTEIN KINASE AND PHOSPHATASE INHIBITORS AND METHODS
FOR DESIGNING THEM

<130> 19226/2152

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<150> 60/336,191

<151> 2001-10-22

<150> 60/410,726

<151> 2002-09-13

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<221> PEPTIDE

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<220>

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PCT/US02/33660

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1 5

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pentapeptide scaffold

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Ile Xaa Gly Glu Phe
1 5

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<223> Description of Artificial Sequence: Boronic
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1 5

<210> 5

<211> 7

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PCT/US02/33660

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Leu Arg Arg Ala Ser Leu Gly

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<223> Description of Artificial Sequence: Peptide
substrate for Src

<400> 7

Gly Ile Tyr Trp His His Tyr

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5

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/33660

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07D 209/14, 215/14; A61K 31/404, 31/47

US CL : 548/495; 546/174; 514/311, 419

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 548/495; 546/174; 514/311, 419

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
CAS ONLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 96/35805 (INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE) 14 November 1996, page 29, lines 11-18 and page 189, lines 9-15.	1-16

☐ Further documents are listed in the continuation of Box C.

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document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

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document member of the same patent family

Date of the actual completion of the international search

03 December 2002 (03.12.2002)

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

Box PCT

Washington, D.C. 20231

Facsimile No. (703)305-3230

Date of mailing of the international search report

02 JAN 2003

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